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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

algorithm Smith-Waterman search, using - protein database protein MPsrch_pp

MasPar time 7.68 Seconds 85.373 Million cell updates/sec Tue Aug 17 16:04:59 1999; Run on:

not generated. output Tabular

>US-09-049-847-4 (1-13) from US09049847.pep 104 1 KFLAVWKITYKDT 13 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

residues 50406085 411786 seqs, Searched:

summaries Post-processing:

Minimum Match 0% Listing first 45

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92 18:U93 19:NEWP 20:NEWU6 21:NEWU8 22:NEWU9 Database

0.310 scale Mean 20.174; Variance 65.147; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	, .	.22e-0	.74e-0	1.74e-01	.74e-0	.74e-0	.28e+0	.14e+0	.14e+0	.42e+0	.42e+0	.42e+0	.42e+0	,33e+0	.33e+0	.33e+0	.33e+0	9.33e÷01	1.47e+02	₹.	1.47e+02	1.47e+02
	Description		equence 5, Appli	Sequence 5, Applicatio	, Appl	equence 3, Applicat	equence 2, Applicati	= 11, App	equence 11, Applicat	equence 6406, Applic	equence 375, Appli	equence 375, Applica	equence 4683, Applic	equence 5353, Appli	equence 25, Applicat	equence 21, Applicat	equence 25, Applicat	227, Applic	equence 11, Appli	ce 112, Applica	e 112, Ap	, Applica
SUMMARIES	ID	1 1 1	-08-39	US-08-575-	-08-46	L0-60-S	S-08-46	-70	S-09-18	S-09-13	CI-US9	S-08-85	S - 09 - 1	S-09-13	S - 09 - 25	-08 - 81	- 92	-09-10	8-7	$\boldsymbol{\omega}$	0-	US-09-288-
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Recombinant Adenylate Cyclase Toxin
Inducing Specific Immune Responses
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ce 5, Application bc,
(AL INFORMATION:
(AL INFORMATION:
PLICANT: Ladant, Daniel
PLICANT: Leclerc, Claude
PLICANT: Sebo, Peter
'ANT: Ullmann, Agnes
'ANT: Ullmann, Agnes
'TON: Specific Immune Responses
'TON: Specific Immune Responses
'Serr
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                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495-0109-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
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                                GENERAL ....

APPLICANT: Ladant, ....
APPLICANT: Sebo, Peter
APPLICANT: Sebo, Peter
APPLICANT: Ullmann, Agnes
TITLE OF INVENTION: Recombinant Mutarithe OF INVENTION: Specific Immune
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ANDRESSEE: Finnegan, Henderson, Fa
                                                                                                ADDRESSEE: Finnegan, Henderson, Fan
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,204
                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,795
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
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Pred. No.
2; Misma
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1613 MW; 1
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34.6%;
ttive
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APPLICANT: Fayolle, C APPLICANT: Ladant, Da APPLICANT: Leclerc, C APPLICANT: Ullmann, A IITLE OF INVENTION: R
                                                                                                                                                                                                                                                                                                                   : 13 amino amino amino amino acid
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SEQUENCE 13
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GENERAL INFORMATION:
APPLICANT: GENGOUX, CHRISTINE; Leclerc, CLAUDE
TITLE OF INVENTION: ANTIGEN-CARRYING
TITLE OF INVENTION: MICROPARTICLES AND THEIR USI
TITLE OF INVENTION: INDUCTION OF HUMORAL OR CELI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/575,879
FILING DATE: 22-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0109-05000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLAUDE
                                                                                                                                                                                                                      Version
                                       Farabow,
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d. No. 1.74e-01;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \Xi
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, FaraDDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASC II
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,021
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S.S: 5

ADDRESS:

BIERMAN & MUSER

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FC

MEDIUM TYPE: FC

MEDIUM TYPE: FC

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LENGTH: 13 amino acids
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R SEQ ID NO:
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1613 MW; 1
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11; Conservative
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TOPOLOGY: lin
MOLECULE TYPE:
SEQUENCE 13 AA; 1
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                                                                                                                 Sequence 2, App. GENERAL INFORMAPPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: GENGOUX, CHRISTINE
APPLICANT: GENGOUX, CHRISTINE
APPLICANT: LECLERC, CLAUDE
TITLE OF INVENTION: ANTIGEN-CARRYING MICROPARTICLES AND THEIR USE IN TILLE OF INVENTION: INDUCTION OF HUMORAL OR CELLULAR RESPONSES
FILE REFERENCE: 102.162-1
CURRENT APPLICATION NUMBER: US/09/076,646
CURRENT FILING DATE: 1998-05-12
EARLIER APPLICATION NUMBER: US 08/397,286
EARLIER FILING DATE: 1995-04-28
EARLIER FILING DATE: 1993-09-13
EARLIER FILING DATE: 1993-09-13
EARLIER FILING DATE: 1992-09-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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L. No. 1.74e-01;
Mismatches 0;
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1.74e-01;
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                      APPLICATION NUMBER: 08/397,286
FILING DATE: 10-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00876
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/92/10879
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 102.162-CON
TELEPHONE: 212-661-8000
TELEPHONE: 212-661-8002
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENDENT: 13
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Pred. No.
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No.
                                                                                                                                                                                                                                                                                                                                                                                    Application US/09076646
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 06-JUN-1995
: 424
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FILING DATE: 06-JUN-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 10-MAR-19
                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                     UNKNOWN
E: PEPTIDE
; 1613 MW; 1
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larity 84.6%;
Conservative
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AA; 1613 MW;
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larity 84.6%;
Conservative
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Local Similarity
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11; Conser
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ORGANISM: PULL
TYPE 13 AA;
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Weeks-Levy, Carolyn L.
VENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
VENTION: CDNA
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                                                               2206 AA.
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Pred. No. 1.28e+00;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 P.
ER: 28,678
TEMPER: 36607-E-PCT-US
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE 2206 AA; 246209 MW; 25431833 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-E-PC:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence 11, Application US/08701191A GENERAL INFORMATION:
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                                                               PRI
                                                                                                                                                                                         2, Application US/08465250 INFORMATION:
                                                                                                                                                                                                                          Vincent
                                                                                                                                                           2, Application US/08465250
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SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER &
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9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
GY: linear
                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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133
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US-09-049-847

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e 70; DB 15;
No. 1.14e+01;
Mismatches 3
                                  COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,809
FILING DATE: November 9, 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/701,191
FILING DATE: August 21, 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 238/091
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: 67-2510
                                                                                                                               2.0
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37050 MW; 551831 CN;
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Pred. No.
1; Misma
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; 28938 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (213) 955-0.
TELEX: 67-3510
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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Local Similarity 66.7%;
les 8; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: prote
                            California
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           CITY: LO STATE: C COUNTRY:
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SEQUENCE 76
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Best Local S
Matches
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APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SAQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETE, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: Moosa Mohammadi
APPLICANT: Joseph Schlessinger
APPLICANT: Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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1.14e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                  **LEFERENCE/DOCKET NUMBER: 32,327

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
37050 MW; 551831 CN;
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No.
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Pred.
1; M
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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FNCE 322 AA;
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ID US-09-188-8
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Best Local
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                           Sequence 6406, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 6406
LENGTH: 76
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                    e 62; DB 16;
. No. 7.42e+01;
Mismatches 3
6406, Application US/09134000A
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Pred. No.
2; Misma
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NUCLEIC ACID AND AMINO ACID:
ENTEROCOCCUS FAECIUM FOR:
DIAGNOSTICS AND THERAPEUTICS
S: 7308
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Pred. No. 7.42e+01
2; Mismatches
                                                                                                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                      207A
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                                                                                                                Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4683, Application US/09107532 GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm a TITLE OF INVENTION: NUCLEIC ACID AITITLE OF INVENTION: ENTEROCOCCUS FITILE OF INVENTION: DIAGNOSTICS AND NUMBER OF SEQUENCES: 7308
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 89,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09107532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CN;
          Application US/08858207A
                                   US/08858207
                                                                                                                                                 Beecham
Road
                                                                                                                                                                                                                                                               FastSEQ for Windows
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/01767
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                              equence 375, Application US/08858
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: Novel Comp
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecha
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68279
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                                                                                                                                                                                                                   COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: Faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                        ZIP: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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                                                                                                                                                                                                                                                                                               FILING DATE: 09-MAY-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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13251
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SEQUENCE 111 AA;
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ID US-09-107-532-4683
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KFLAVWKITY
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CITY: K
STATE:
            375,
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                                 Sequence
GENERAL
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             Sequence
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Best Local
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7.42e+01;
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                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version
RRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07950
FILING DATE: 14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                             e 375, Application PC/TUS9707950
L INFORMATION:
ICANT: Black, Michael
ICANT: Hodgson, John
ICANT: Knowles, David
ICANT: Nicholas, Richard
ICANT: Stodola, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                        PRT;
                                                                                                                                                                                                                              Compounds
                                                                                                                        Application PC/TUS9707950
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68279 CN;
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3R: P50475
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Road
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                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                              Novel
552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 amino acids
amino acid
DNESS: single
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9 Swedeland D
of Prussia
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13251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.6%;
( 60.0%;
ervative
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                             Sequence 375, Application GENERAL INFORMATION:
APPLICANT: Black, Mic APPLICANT: Hodgson, U APPLICANT: Knowles, I APPLICANT: Nicholas, APPLICANT: Stodola, F TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: C.S. SIRANDEDNESS: SI
                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                         ADDRESSEE: Sr
STREET: 709 (
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6; Conser
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SEQUENCE 111 AA;
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                        e 61; DB 16; Le
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Mismatches 2;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, v
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W; 2000477 CN;
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,68:
FILING DATE:
                                                                                                                                                                                                   equence 25, Application US/09253682
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CY
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/926,922

FILING DATE: September 10, 1997

ATTORNEY/AGENT INFORMATION:

NAME: CSerr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: AVIR 1:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-839-7810
                                                                                                                          PRT
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                       Score 61;
Pred. No.
2; Misma
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er 10, 1997
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Pred.
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    34784
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STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 642 amino acid
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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Larity 63.6%;
Conservative
    9450 MW;
                       Similarity 53.6%, 7; Conservative
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LOCATION: 1..642
OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 5353
LENGTH: 80
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                                                                                                                       PRICATION NOTA:
PRICATION NUMBER: 60/085598
FILING DATE: MAY 14, 1998
FILING DATE: MAY 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 4683:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                    DATA:
R: US/09/107,532
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
STREET: 100 Beaver Street
CITY: Waltham
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70613 MW; 2071988
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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ORGANISM: Enterococcus faecalis
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                                        Massachusetts
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Best Local Similarity 54.5%;
Matches 6; Conservative
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CURRENT APPLICATION DA
APPLICATION NUMBER:
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ORGANISM: Ent
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                  STREET:
CITY: Wa
STATE: M
COUNTRY:
ZIP: 023
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LOCATION:
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Sequence 21, Application US/08812716
GENERAL INFORMATION:
APPLICANT: KEMBLE, George
APPLICANT: DUKE, Gregory
APPLICANT: SPAETE, Richard
TITLE OF INVENTION: VIRULENCE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: AVIRON
STREET: 297 N. Bernardo Avenue
CITY: Mountain View
STATE: California
COUNTRY: USA
ZIP: 94043
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ZIP: 94043

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,716
FILING DATE: 06-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 44,587
FILING DATE:
ALTING DATE:
APPLICATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: AVIR-5032
TELECOMMUNICATION INFORMATION:
TELEFAX: 650.919.6637
TELEFAX: 650.919.6937
TELEFAX: 650.919.6937
TELEFAX: 650.919.6937
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                          STANDARD;
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US-08-812-715-21
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Indels Score 61; DB 13; L. Pred. No. 9.33e+01; 2; Mismatches 2; Query Match Best Local Similarity 63.5%; Matches 7; Conservative 414 4 LAIWQRIYNDT 41. ||:| ||:|| 3 LAVWKITYKDT 13 404 ă

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- protein database search, using Smith-Waterman algorithm protein MPsrch_pp

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>US-09-049-847-3 (1-12) from US09049847.pep 82 1 GQIGNDPNRDIL 12 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

seqs, 50406085 residues 411786 Searched:

Minimum Match 0% Listing first 45 Post-processing:

summaries Database:

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1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B
10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92
18:U93 19:NEWP 20:NEWU6 21:NEWU8 22:NEWU9

scale 0.400 Variance 44.259; Mean 17.684; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	,	Pred. No.	5.59e-0	596-0	.59e-0	1	.59e-0	.80e+0	.80e+0	.14e+0	.14e+0	.14e+0	.14e+0	.14e+0	14	.14e+0	.14e+0						
	•	Description	equence 46, Applica	equence 3, Applicati	equence 46, Applicat	quence 46, Applic	equence 7, Applicati	equence 6, Applicati	equence 6, Applicati	equence 6, Applicati	equence 22, Applicat	equence 511, Applica	equence 1, Applicati	eguence 1938 <u>2</u> , Appli	equence 19382,	eguence 20, Applicat	equence 11, Applicat	equence 18, Applicat	equence 14, Applicat	equence 32, Applicat	equence 1, Applicati	equence 17, Applicat	equence 35, Applicat
SUMMARIES	í H	1D 	PCT-US98-0	9-04	-32	9-6	-08-78	S - 08 - 48	S-08-48	S-08-30	8-12	80-60-8	-08 - 91	60-09-S	ı	S-08-37	S-08-37	-08-08	-08-26	9-26	-08-31	-08-56	
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SOFTWARE: FastSEQ f
SEQ ID NO 46
LENGTH: 12
TYPE: PRT
ORGANISM: Clostriċ
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SEQUENCE 12 AA;
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GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Leclerc, Claude
APPLICANT: Lo-Man, Richard
TITLE OF INVENTION: Mutiple antigen alycopeptide ca
TITLE OF INVENTION: Comprising the same and use the
FILE REFERENCE: 102.166A
CURRENT APPLICATION NUMBER: US/09/049,847
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/041,726
EARLIER FILING DATE: 1997-03-27
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Mismatches 0
                               e 82; DB 1; L
No. 5.59e-03;
Mismatches 0
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GENERAL INFORMATION:
APPLICANT: Lunsford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MICROPARTICLES FOR DELIV
FILE REFERENCE: 08191/014001
CURRENT APPLICATION NUMBER: US/09/321,346
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: US 09/266,463
EARLIER FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 114
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I. No. 5.59e-03;
Mismatches 0
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                                          e 82; DB 18;
.. No. 5.59e-03;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09003253
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FC
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
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ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Ventron APPLICATION DATA:

APPLICATION NUMBER: US/09/003,25:
FILING DATE: 06-JAN-1998

CLASSIFICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/035,983

FILING DATE: 22-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Ph.D., J.D., Janis

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/01

TELEPHONE: 617/542-8906
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Pred. No.
0; Misma
                                          Score 82;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                     US/09003253
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tetanii
V; 550 CN;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
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                                            100.0%;
larity 100.0%;
Conservative
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Similarity 100.0%;
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Version

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Grey, How...
Sidney, John
: Alexander, Jeffery L
: Del Guercio, Marie-France
INVENTION: Alteration of Immune Re
INVENTION: DR-Binding Peptides
INVENTION: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 82; DB 9; L
. No. 5.59e-03;
Mismatches 0
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,218
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,871
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-62-2
                                                                                                                                                              Townsend a
a, Steuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
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Pred. No.
  Sequence 6, Application US/08485218
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffery L
APPLICANT: Del Guercio, Marie-Fr
TITLE OF INVENTION: Alteration o
TITLE OF INVENTION: Alteration o
TITLE OF INVENTION: Alteration o
TITLE OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townser
STREET: One Market Plaza, Steur
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26 MW; 637 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 415-543-9600 TELEFAX: 415-543-5043 IFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sette, Alessandro
Gaeta, Federico
                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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larity 100.0%;
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GENERAL INFORMATION:
APPLICANT: Sette, A.
APPLICANT: Gaeta, Fe
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CITY: S
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GENERAL INFORMATION:
APPLICANT: Alexander, Jeffrey L.
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Desired Determinants
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Desired Determinants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
SIREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTR: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,822A
FILING DATE: 23-JAN-1997
CLASSIFICATION NUMBER: US 60/010,510
FILING DATE: Z4-JAN-1996
ATPORNEY/AGNI INFORMATION:
NAME: Bastian Kerin I
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Pred. No.
0; Misma
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACIERISTICS:
                                                                                                                                Application US/08788822A
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Kevin L.
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Conservative
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GQIGNDPNRDIL
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APPLICANT: Sette, Alessandro

APPLICANT: Gaeta, Federico

APPLICANT: Grey, Howard M.

APPLICANT: Sidney, John

APPLICANT: Alexander, Jeffrey L.

TITLE OF INVENTION: Alteration of Immune Response Using

'TITLE OF INVENTION: DR-Binding Peptides

NUMBER OF SEQUENCES: 17
                                     Using
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                                     Response
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Eighth Floor
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|. No. 5.59e-03;
| Mismatches 0;
 LICANT: Grey, Howard M.
LICANT: Sidney, John
LICANT: Alexander, Jeffery L.
LICANT: Del Guercio, Marie-France
LE OF INVENTION: Alteration of Immune Re
LE OF INVENTION: DR-Binding Peptides
BER OF SEQUENCES: 31
                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                  NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 018623-006220US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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14-SEP-1994
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                       Townsend
Center, E
                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,21
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                   Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08305871
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08305871
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  637 CN;
                                                                     Two Embarcadero C
San Francisco
California
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APPLICANT: Grey, Howard APPLICANT: Sidney, John APPLICANT: Alexander, Je APPLICANT: Del Guercio, TITLE OF INVENTION: Alte ITTLE OF INVENTION: DR-E NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    FILING DATE: 07-JUN-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-SEP-19
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larity 100.0%;
Conservative
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                                                                                                       COUNTRY: USA
ZIP: 94111-3834
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                                  Crew LLE
th Floor
         ADDR.
STREET:
CITY: San Fr.
STATE: Californ.
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
TRATING SYSTEM: PC-DOS/MS-DOS
TRATION DATA:
TATION DATA:
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. No. 5.59e-03;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-62
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08121101
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: GAETA, Federico
APPLICANT: GREY, Howard M.
APPLICANT: SIDNEY, John
TITLE OF INVENTION: ALTERATION OF
TITLE OF INVENTION: DR-BINDING PEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82;
Pred. No.
0; Misma
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Kevin L.

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ONDENCE ADDRESS:
SSEE: Townsend and I
I: Two Embarcadero C
San Francisco
: California
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CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŋ
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
larity 100.0%;
Conservative
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STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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ses 12; Conse
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Sequence 19382, Application US/60096409A
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-016P
CURRENT APPLICATION NUMBER: US/60/096,409A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 19382
LENGTH: 373
                                                                                                                         FUNCTIONAL FRAGMENT ANTIGEN AND
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                                                                                                                                                                                                                                                                                                                                                                                      373
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. No. 4.80e+01;
Mismatches 3
                                                                                   Sequence 1, Application US/08913880
GENERAL INFORMATION:
APPLICANT: MATSUDA, Morihiro
TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL
TITLE OF INVENTION: VACCINE
FILE REFERENCE: 216-380P
CURRENT APPLICATION NUMBER: US/08/913,880
CURRENT FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
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Pred. No.
2; Misma
                                                                US/08913880
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1315 AA; 150681 MW;
                                                                                                                                                                                                                                              MW;
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SEQUENCE 373 AA; 41473 MW;
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100.0%;
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ID US-60-096-409-19382
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GQIGNDPNRDIL
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LENGTH: 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 511, Application US/09082279
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7853-043
CURRENT APPLICATION NUMBER: US/09/082,279
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1436
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 511
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
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. No. 5.59e-03;
Mismatches 0
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                                                                                                                                                                                                                                                     e 82; DB 5;
. No. 5.59e-
Mismatches
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,10:
FILING DATE: 14-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-6:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
TENGTH: 14 amino acide
       #1.0,
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903 CN;
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09082279
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Pred.
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                                                                                                                                                                                                                                                                            0
                                                                                                                                               LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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100.08;
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Best Local Similarity 100.0%;
Matches 12; Conservative
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ORGANISM: Artificial 8
FEATURE:
OTHER INFORMATION: Cox
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14 AA; 1589
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12; Conser
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ID US-08-913-880-1
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US-09-082-
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. No. 1.14e+02;
Mismatches 3
               •= (17)
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e 50; DB 7; L
. No. 1.14e+02;
Mismatches 3
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R: 022650-263
                                                                                                                                                                                                                                                                      Paul
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COUNTRY: ULL
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMPUTER: IBM PC compatible
TOMPUTER: TSM PC COMPATIBLE
TOMPUTER: TSM PC COMPATIBLE
TOMPUTER: TSM PC COMPATIBLE
TOMPUTER: ASSTEM: PC-DOS/MS-DOS
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19-JAN-1995
                                                                                                                                                                                                                                                                    Marcel Pa
ENCODING
                                                                                                                                                                                                                                                                                                                 Swecker
                                                                                                                                                                                                         Sequence 11, Application US/08374888
GENERAL INFORMATION:
APPLICANT: HALL, Linda M
APPLICANT: REN, Dejian
APPLICANT: ZHENG, Wei
APPLICANT: DUBALD, Manuel Marcel Particle OF INVENTION: GENES ENCODING
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (genomic)
MW; 945243 CN;
                                                                                                                  PRT,
 Score 50;
Pred. No.
3; Misma
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                                                                                                                                                                                     Application US/08374888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 0226
TELECOMMUNICATION INFORMATION:
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Pred.
3; M
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     E ADDRESS:
Burns, Doane,
O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acids
                                                                                                                  STANDARD;
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SOFTWARE: Patentin Re-
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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Conservative
 61.0%;
larity 50.0%;
Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          STREET: P.O. BOX CITY: Alexandria STATE: Virginia
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MOLECULE TYPE:
UENCE 432 AA;
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            Similarity
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                                               GQAGAEPSRDSM
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US-08-374-888-11
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                                               CANDIDA
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          Sequence 19382, Application US/09248796
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 19382
LENGTH: 373
TYPE: PRT
ORGANISM: Candida albicans
                                               0
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium Channel
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                                                                                                                                                                                     Score 53; DB 17; L/
Pred. No. 4.80e+01;
2; Mismatches 3;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08374888A
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Loubald, Manuel Marcel Pau
TITLE OF INVENTION: Genes Encoding a
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER &
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,888A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paul
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1952 MW; 1883
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AME: McGowan, Malcolm M
EGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                    : Candida albicans
373 AA; 41473 MW;
                                                                                                                                                                                     Similarity 58.3%; 7; Conservative
                                                                                                                                                                                                                                    194
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GQIGNDPNRDIL
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US-08-374-888A-20
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

algorithm Smith-Waterman using search, database protein protein MPsrch_pp

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>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Title: Description: Perfect Score:

Sequence:

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residues 21266608 seds, 170751 Searched

08 45 Match first Minimum Listing Post-processing:

Database

summaries

geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed; derived by analysis of the total score distribution. score and is Pred

0.296

scale

73.372;

Variance

21.709

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SUMMARIES

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Result No.	ore	Query Match	Lengt	DB	ID	Description	Pred. No
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7	158	100.0	21	N		THE TOTAL STREET	340-0
m	S	00.			6703	etanus toxin fradm	340-0
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9	Ω	00			8839	-cell antiden TT3	340-0
_	ហ	00.			7322	etanus toxoid enit	340-0
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anus toxin help	elper I cell epito	tanus toxin helper	GE CH4 region cont	GE CH4 region contd	niversal helper T-c	anus toxin frag	-cell stimulatory	etanus toxoid prot	etanus toxoid prot	arrier peptide for	lostridium botul	mmunogenic type F	mmunogenic type F	lostridium botulin	lostridium botulin	um botulin	ecombinant botulin	lostridium botulin	ype A neurotoxin C	lostridium botulinu	lostridium botulin	ype A neurotoxin C	Tostridium botuli	. botulinum type A	lostridium botulinu	lostridium botulin	artial sequence of	on-structural pr
8257	R62693	0560	8259	8356	7132	6927	3543	7883	7883	0300	6840	0901	0901	6839	6839	6839	5601	6839	9500	6838	6833	9500	6839	9501	6839	6839	5654	1183
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ALIGNMENTS

RESULT 1

ID W67579 standard; peptide; 21 AA.

AC W67579.

AC W67579.

DE W67579.

DE T-cell epitope peptide #5 for chimeric fimbrin/T-cell epitope peptide.

KW Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;

KW Minunogenic composition; immune response.

Synthetic.

BN USS843464-A.

PD 01-DEC-1998.

PR 02-JUN-1995; 460502.

PR 02-JUN-1995; US-460502.

PR 03-JUN-1995; US-460502.

PR 03-JUN-1995; US-460502.

PR 04-14-14-14-14.

PR 1 Synthetic chimeric fimbrin peptide - useful for vaccination against Disclosure; Column 4; IGPP; English.

CC comprising a non-typable Haemophilus influenzae fimbrin peptide is CC used in immunogenic compositions which induce an immunogenic compositions with induced in immunogenic compositi

Gaps ö Length 21; Indels ·· 0 Score 158; DB 38; Pred. No. 4.34e-09 0; Mismatches (Query Match Best Local Similarity 100.0%; Matches 21; Conservative

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21 g Q

2 standard; peptide; LT 2 R11896 stand R11896; 19-JUL-1991 Immunogenic RESULT ID RI AC RI DT 15

AA

(first entry) conjugate constituent peptide, TT3

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T-cell epitope.
Clostridium tetani
                                                                                                                                                                                                                                                                                                            standard;
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                                                   Match
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Best Local
Matches
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W67034.

W67034.

W67034.

IS-DEC-1998 (first entry)

Fetnus toxin; vaccine, antibody: carbohydrate peptide conjugate;

Gentlement poly-lysine; epitope: tumour.

Gentlement poly-lysine; epitope: temour.

For your poly-lysine; epitope: temour.

For your poly-lysine; epitope: temour.

For your poly-lysine; poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: the proposition of the comprises a carrier with adendiment poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an enthopy puritied from biological fluid or calls of organisms administered with the carbohydrate peptide conjugate, antibody and enthopy artities from biological fluid or calls of organisms administered with the carbohydrate peptide conjugate, antibody and enthopy purities from biological fluid or calls of organisms administered with the carbohydrate peptide conjugate, where the carbohydrate peptide conjugate, which the carbohydrate peptide conjugate, which the carbohydrate peptide conjugate, which the carbohydrate peptide conjugate stimulates of support an immune response of an persent sequence contrapped to tumours. They can be used to enhance and animals against bacterial infections against virus, they can be used to enhance and animals against bacterial infections caused by hepatitis virus, HIV or oytomegalo conjugate stimulating undesired immune responses, Inc composition in response without stimulating undesired immune responses, Inc composition in casponses, of humans and animals against bearing humans and signals. The year as equence contrapported to minimals and epitope in a carbohydrate peptide conjugate stimulates to residues 947-967 of tetanus of conium and peptide conjugate stimulating conference again
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                        falciparum

Claim 1; page 13; 16pp; English.

Claim 1; page 13; 16pp; English.

This peptide corresps. to residues 947-967 of Tetanus toxin. It can be used as a universal carrier for the prepn. of an immunogenic conjugate. It is covalently bound to a peptide or polysaccharide conjugate. It is covalently bound to a peptide or polysaccharide conjugate can be used as a vaccine for malaria. This peptide is recognised by different T-contains 2 epitopes: (a) 953-967, recognised by DR5-restricted clones; and (b) 947-960, recognised by all other DR and DP-crestricted clones.

Crestricted clones.

Sequence 21 AA;
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Plasmodium
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                                                                                                      active fragment (claimed)
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Pred. No. 4.34e-09;
                                                                                                                                                                                                                                                                                                                carriers
s against
  histocompatibility
                                                                                                                                                                                                                                                           Pianchi E, Pessi A, Corradin G;
WPI; 91-141874/20.
Synthetic peptide(s) used as universal c
immunogenic conjugates used as vaccines
                                                    Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                              EP-427347-A.
15-MAY-1991.
07-NOV-1990; 202948.
10-NOV-1989; IT-022355.
(ENIE) ENIRICERCHE SPA.
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/label= (
     vaccine; major
                            toxin
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Bianchi
WPI; 91-
                            Tetanus
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lein; CETP; cholesteryl ester;
very low density lipoprotein; VLDL,
cell epitope; antibody;
d range helper T cell epitope;
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levels,
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Claim 11; Page 43; 72pp; English.
A helper T-cell epitope (W06130) comprises amino acids 947-967
of tetanus toxoid protein. It can be utilised in novel peptide
vaccines (see also W06129, W06132) also including B-cell
epitope(s) from human or rabbit cholesteryl ester transfer
protein (CETP) to elicit an immune response against endogenous
CETP activity, thereby treating or preventing a cardiovascular
disease, such as atherosclerosis.
Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          '-cell epitope.
Ter protein; CETP; antigen; vacciantherosclerosis; tetanus toxoid
                                                                               Indel
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DB 36;
Mo. 4.34e-09;
Mismatches
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Pred. No. 4
                 Score 158;
Pred. No. 4
0; Mismat
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W46449;
18-MAY-1998 (first entry)
Broad range helper T cell epitope from Cholesteryl ester transfer protein; CF high density lipoprotein; HDL; very Land low density lipoprotein; LDL; T cell on DNA plasmid-based vaccine; broad rang transfer transfer.
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WO9634888-A1.

07-NOV-1996.

01-MAY-1996; U06147.

01-MAY-1995; US-432483.

'TCEL-) T CELL SCI INC.
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100.0%;
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Tetanus toxoid protein T-ce
Cholesteryl ester transfer
cardiovascular disease; ath
                       100.08;
100.08;
                                                                                                                                          Conservative
                                                 Similarity 100.0% 21; Conservative
                                                                                                                                                                                                                                                                                                                         Peptide;
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Clostridium tetani.
W09741227-A1.
06-NOV-1997.
01-MAY-1997; US-802967.
21-FEB-1997; US-802967.
01-MAY-1996; US-640713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope - used to decreasing the risk
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The present sequence represents a broad range helper T cell epitope of the tetanus protein. It can be used in DNA plasmid-based vaccines against cholesteryl ester transfer proteins (CETPs). CETPs mediate the transfer of cholesteryl esters from high density lipoprotein (HDL) transfer of cholesteryl esters from high density lipoprotein (HDL) and vice versa. An increased CETP activity produces an atherogenic lipoprotein profile and induces atherosclerosis. A DNA plasmid-based cipoprotein profile and induces a least one B cell epitope of CETP cipoprotein frame with at least one segment encoding a broad range helper cipoprotein from a loope. The vaccines can be used to elevate the ratio of circulating HDL to circulating LDL, VLDL or total cholesterol in a human. The vaccine can be used to produce anti-CETP antibodies in vivo and for treating cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for antibody prodn.

Claim 7; Page 62; 95pp; English.

Claim 7; Page 62; 95pp; English.

Claim 7; Page 62; 95pp; English.

This T-cell antigen TT3 peptide may be attached to a core peptide contained in one of the 2 subunits of an alpha-helical coiled-coil heterodimer. Each core peptide is comprised of terminal and internal AA repeat sequences. This peptide antigen is attached to the core peptide through covalent linkages to certain AA of the internal repeats. The 2 subunits of the heterodimer are arranged in a stable alpha-helical coiled-coil configuration having a 1:1 stoichiometry, and the peptide antigen is disposed toward the outer surfaces of the configuration. The heterodimer may be used as a synthetic vaccine (optionally multivalent) or to generate
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-lymphocyte;
core peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coiled-coil
                                                                                                                                                                                                                                                                              e 158; DB 28; L
|. No. 4.34e-09;
| Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 158; DB 17; Pred. No. 4.34e-09; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hetero:dimeric polypeptide immunogen in with different antigens on each sub:unit for antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R88397;
12-JUN-1996 (first entry)
T-cell antigen IT3 peptide.
T-antigen; vaccine; antibody; T-cell; T-alpha-helix; coiled-coil heterodimer; cc Synthetic.
W09531480-Al.
23-NOV-1995.
18-MAY-1995.
18-MAY-1995; CA0293.
18-MAY-1994; US-245507.
(SPIS-) SPI SYNTHETIC PEPTIDES INC.
Cachia PJ, Hodges RS, Houston ME, Irv Zhou NE;
WPI; 96-010880/01.
                                                                                                                                                                                                                                                                          Score 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain antibody;
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Similarity 100.0%;
21; Conservative
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Best Local Similarity 100.0%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
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Multispecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W73222 stand
W73222;
25-JAN-1999
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Sequence
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Matches
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R88397
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Example 7; Column 27; 57pp; English.

This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal growth factor receptor (EGFR), comprises contacting the tumour cell with a multispecific protein molecule (preferably a single chain antibody) comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can be used for treating cancers especially be administered prophylactically to vaccinate a subject against infection by a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                   infection
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R62702;
10-SEP-1995 (first entry)
LHRH-containing immunogenic peptide.
Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cel
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                                                                                                                                                                                                                                                                    multi-specific molecule a portion which binds
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Synthetic immunogenic peptides are provided in which a universal stimulator is linked to a peptide or protein hapten containing B and/or cytotoxic T lymphocyte epitopes, giving a product which capotent immune responses to the coupled peptide or protein. The potent immune responses to the coupled peptide in member stimulator consists of (A) a promiscuous helper I cell epitope (T which elicits an immune response to the coupled peptide in member
                                             cancer
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0
                HER 2/neu;
ovarian ca
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                                      cancer;
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                    ADCC;
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4.34e-09;
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                llar cytotoxicity;
receptor; breast o
                                                                                                                                                                                                                                                                   ls - using
antibody a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158;
antibody-ucr-
epidermal growth fact.
Synthetic.
US5837243-A.
17-NOV-1998.
07-JUN-1996; 661052.
07-JUN-1995; US-661052.
18 (MEDA-) MEDAREX INC.
1990 PO23374/02.
Theo YM, Goldstein J, Graziano R, Scholis Pocific Killing of tumour cells -
comprising an anti-Fc receptor anti-
a target cell
Theorem Synthems Synthy Englis
Theorem Synt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "LHRH hapten"
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100.0%;
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/note=
23..32
/note=
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28-APR-1994; U04832.
27-APR-1994; US-057166.
14-APR-1994; US-229275.
(LADD/) LADD A E.
(WANG/) WANG C Y.
(ZAMB/) ZAMB T.
Ladd AE, Wang CY, Zam WPI; 94-357910/44.
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Matches
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WPI: 91-297504/41.

NWPI: 91-297504/41.

The national falciparum

S claim 10: Page 15: 22pp; English.

C each of the alpha and epsilon amino groups

is substituted by Lys, both of the latter

two Lys residues being substituted in each

of their alpha and epsilon amino groups by

(NANP)60YIKANSKFIGITEFNNFTVSFWLRVPKVSASHLE"

The peptide is a specific example of highly generic

immunogenic substituted lysines or polylysines having a number n

c where n is 1-15) of L-lysine amino acid residues of alpha and

epsilon amide linkage, where (n+1)/2 of the alpha amino groups

and/or (n+1)/2 of the epsilon amino groups are substituted with

polypeptides consisting of one or more plasmodial B epitopes

covalently bound to one or more peptides with an amino acid sequence

corresponding to that of a T epitope such as FNNFTVSFWLRVPKVSASHLEA

C OT LYTEANSKFIGITE.

The best of a polyber of imminogenes for manney for the best of a polyber of
                                                                                                                                                                                                                                                                                                                                                                          ;
a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component. The present sequence represents an LHRH-containing, invasin-free immunogenic peptide as above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-dependent carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis, benign uterine tumours, recurrent functional ovarian cysts, (severe) chancetion of infertility.
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            (B)
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61
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both alpha and epsilon amino groups are
substituted with the sequence
(NANP)6QYIKANSKFIGITEFNNFTVSFWLRVPKVSASHLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for antimalarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l as immunogens for antimalaria vaccines
                                                                                                                                                                                                                                                                                                                                  Length 32;
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Pred. No. 4.34e-09
0; Mismatches
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/label= T epitope
39..59
/label= T epitope
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
branched polypeptides
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-1990; IT-019914.
) ENIRICERCHE SPA.
) ----hi E, Corradin G
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larity 100.0%;
Conservative
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Synthetic.
Key
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Pessi A, Bianchi E
WPI; 91-297504/41.
                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 21; Conser
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09-OCT-1991.
28-MAR-1991;
02-APR-1990;
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R14263 stand:
R14263;
14-JAN-1992
Immunogenic ]
                                                                                                                                                                                                                                                                                             Sequence
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Claim 8; Page 15; 22pp; English.

The peptide is a specific example of highly generic
immunogenic substituted lysines or polylysines having a number n
(where n is 1-15) of L-lysine amino acid residues of alpha and epsilon amide linkage, where (n+1)/2 of the alpha amino groups and/or (n+1)/2 of the epsilon amino groups are substituted with polypeptides consisting of one or more plasmodial B epitopes covalently bound to one or more peptides with an amino acid sequence corresponding to that of a T epitope such as FNNFTVSFWLRVPRVSASHLEA
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See also R14262 - R14265 and R15436.
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                                                                                   Indels
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which both alpha and epsilon amino group
are substituted with the sequence
FNNFTVSFWLRVPKVSASHLE(NANP)10"
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wo. 4.34e-09;
Mismatches
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                                                             DB 3;
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FNNFIVSFWLRVPKVSASHLE(NANP)10
                                                                                   Mismatches
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m antibodies
be effected
5 and R15436.
                                                         Score 158;
Pred. No. 4
0; Mismat
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Pred. No.
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28-MAR-1991, 200727.
02-APR-1990, IT-019914.
(ENIE ) ENIRICERCHE SPA.
Pessi A, Bianchi E, Corradin G
WPI; 91-297504/41.
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 determining anti-Plasmodium
samples. Determination can b
see also R14261-2, R14264-5
Sequence 63 AA;
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Similarity 100.0%;
21; Conservative
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21; Conservative
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ID R14265 standa
AC R14265;
DT 14-JAN-1992
DE Immunogenic k
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}-OCT-1991.
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R14261 stand:
R14261;
14-JAN-1992
Immunogenic ]
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Claim 13; Page 16; 22pp; English.

The peptide is a specific example of highly generic immunogenic substituted lysines or polylysines having a number n (where n is 1-15) of L-lysine amino acid residues of alpha and epsilon amide linkage, where (n+1)/2 of the alpha amino groups and/or (n+1)/2 of the epsilon amino groups are substituted with polypeptides consisting of one or more plasmodial B epitopes covalently bound to one or more peptides with an amino acid seque corresponding to that of a T epitope such as FNNFTVSFWLRVPKVSASHIOU OX QYIKANSKFIGITE.
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against
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                                                            /note= "epsilon amino substituted with the FNNFTVSFWLRVPKVSASHLE(NANP)10K "
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   immunoassay
                                                                                      /note= "epsilon amino substituted walpha and epsilon amino groups are substituted with the sequence FNNFTVSFWLRVPKVSASHLE(NANP)10K"
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. No. 4.34e-09;
Mismatches 0
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 lysine;
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Pred. No. 4
0; Mismat
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VQGEESNDK"
                   Location/Qualifiers
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malaria; ly
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8-MAR-1991; 200727.
2-APR-1990; IT-019914.
ENIE ) ENIRICERCHE SPA.
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larity 100.08;
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Plasmodium; ma
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/label=
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Plasmodium;
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Pessi A, Bianchi I
WPI; 91-297504/41
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09-OCT-1991.
28-MAR-1991;
02-APR-1990;
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Immunogenic
Immunogen;
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R14262 :
R14262;
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preparing genetically non-restricted antimalaria vaccines and for determining anti-Plasmodium antibodies in blood, serum and blood-spot samples. Determination can be effected by ELISA.
See also R14262 - R14265 and R15436.
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09-0CT-1991.

28-MAR-1991; 200727.

ROZ-APR-1990; IT-019914.

(ENIE ) ENIRICERCHE SPA.

Pessi A, Bianchi E, Corradin G;

WPI; 91-297504/41.

New immunogenic branched polypeptide derivs. - used as antigens in enzyme immunoassays and as anti sporozoite vaccines against in enzyme immunoassays and as anti sporozoite vaccines against in enzyme immunoassays and as anti sporozoite vaccines against in epptide is a specific example of highly generic claim 11; Page 16; 22pp; English.

Claim 11; Page 16; 22pp; English.

Claim 11; Page 16; 22pp; English.

Claim 11; Page 16; L-1ysines or polylysines having a number n (where n is 1-15) of L-1ysine amino acid residues of alpha and epsilon amide linkage, where (n+1)/2 of the alpha amino groups are substituted with
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Claim 9; Page 15; 22pp; English.

The peptide is a specific example of highly generic
immunogenic substituted lysines or polylysines having a number n
(where n is 1-15) of L-lysine amino acid residues of alpha and
epsilon amide linkage, where (n+1)/2 of the alpha amino groups
and/or (n+1)/2 of the epsilon amino groups are substituted with
polypeptides consisting of one or more plasmodial B epitopes
covalently bound to one or more peptides with an amino acid seque
corresponding to that of a T epitope such as FNNFTVSFWLRVPKVSASHI
or QYIKANSKFIGITE.
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(NANP)3FNNFTVSFWLRVPKVSASHLE(NANP)10K"
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alpha and epsilon amino groups are eacl
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09-0CT-1991.
28-MAR-1991; 200727.
02-APR-1990; IT-019914.
(ENIE ) ENIRICERCHE SPA.
Pessi A, Bianchi E, Corradin G
WPI; 91-297504/41.
on the alpha a E(NANP)10 and sequence VQG
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14-JAN-1992
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                  n an amino acid sequenc
FNNFTVSFWLRVPKVSASHLEA
                                                          and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                             degeneracy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 50pp; English.

The (G+C) content of the synthetic gene is increased by 47% wrt native sequence. This eliminates six "terminator" regions which were found to be present in (A+T) rich regions. The terminators (termination/endo-nucleolytic processing/polyadenylation sites) were previously responsible for incomplete transcription of the mRNA. The elimination of these elements (using codon degeneracy provided for successful expression in yeast of the tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                yeas
                                                                                                                                                                                                                                                                                                                                                                       the
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polypeptides consistent.

covalently bound to one or more per--
corresponding to that of a T epitope such as Final
corresponding to that of a T epitope such as Final
or OYIKANSKFIGITE.

The branched polypeptides can be used as immunogens for
preparing genetically non-restricted antimalaria vaccines and
determining anti-Plasmodium antibodies in blood, serum and bl
conception can be effected by ELISA.

See also R14261 - R14263, R14265 and R15436.

See also R14261 - R14263, R14265 and R15436.

Connence 77 AA;
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        or more plasmodial B epitopes
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                                                                   serum and
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                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 158;
Pred. No. 4
0; Mismat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                       sequence encoding tetanus toxin :
Ifacture of vaccines for immunity
                                                                                                                                                                                                                                                  βŽ
                                                                                                                                                                                                                                                                    Synthetic.
EP-430645-A.
05-JUN-1991.
27-NOV-1990; 312870.
28-NOV-1989; GB-026832.
17-MAR-1990; GB-006097.
(WELL ) WELLCOME FOUNDATION LTD.
Makoff AJ, Romanos MA, Clare JJ, F
WPI; 91-166115/23.
N-PSDB; Q12121.
                                                                                                                   Score
Pred.
0; M
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ID P70345 standard; Protein; 573 AA.
AC P70345;
DT 22-APR-1991 (first entry)
DE Portion of B fragment and all of
KW TI; vaccine.
OS Clostridium tetani.
PN EP-209281-A.
PD 21-JAN-1987.
PP 27-JUN-1986; 305029.
PR 28-JUN-1985; GB-016442.
PR (WELL) Wellcome Foundation Ltd.
PI Fairweather NF;
DR WPI; 87-015999/03.
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arity 100.0%;
Conservative
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                                                                                                                   Similarity 100.08
21; Conservative
                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                   n fragment vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                          as host organism.
Disclosure, Fig 2
                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                   toxin
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R12471 stand
R12471;
05-AUG-1991
                                                                                                                                                                                                                                                 Tetanus toxi
Terminator;
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fragment
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TUST80024-A.

14-JUL-1998; 668381.

15.21-JUN-1996; 668381.

R 23-JUN-1996; 668381.

R 23-JUN-1996; 668381.

R 23-JUN-1996; US-668381.

R 23-JUN-1996; US-668381.

R 23-JUN-1996; US-668381.

R 21-JUN-1996; US-668381.

R 23-JUN-1996; US-668381.

R 23-JUN-1996; US-668381.

R 21-JUN-1996; US-68
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W48909 standard; Protein; 618 AA.

C W48909;
T 23-SEP-1998 (first entry)
ESOD-1/TTC hybrid protein.
W Chimeric; copper-zinc superoxide dismutase; SOD-1; TTC; SOD:Tet451;
W Chimeric; copper-zinc superoxide dismutase; SoD-1; TTC; SOD:Tet451;
W tetanus toxin fragment C; tetanus holotoxin; nerve cell; stroke;
W neurological disorder; oxidative stress; brain hypoxia-reperfusion;
W epilepsy; Parkinson's disease; Huntington's disease.
SS Chimeric - Homo sapiens.
Chimeric - Clostridium tetani.
Location/Qualifiers
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.34e-09;
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                                                                                      fragment,
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Pred. No. 4.34e
0; Mismatches
                                         for
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                                                                                                            used
                      tetanus t
antigens
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Huntington's
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                                                                                                         host,
sease.
                                                                                   tetanus
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/note= "SOD-1"
168..618
/note= "TTC moi
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                     coding for
to express
p; English.
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"TTC 1
N-PSDB; N70545.
Cloned DNA sequence coding f
contg. epitope used to expre
Claim 4; Fig 1; 36pp; Englis
Gene product comprises a tet
expressed in a transformed h
production, against the dise
Sequence 573 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
Similarity 100.0%;
21; Conservative
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100.0%;
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618 AA;
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Best Local
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Immunogenic luteinising hormone releasing hormone peptide(s) -
that suppress LHRH activity in males and females

Claim 7; Page 25; 213pp; English.

Synthetic immunogenic peptides are provided in which a universal immune

Synthetic immunogenic peptides are provided in which a universal immune

Synthetic immunogenic peptides are provided in which a universal immune

Stimulator is linked to a peptide or protein hapten containing B cell

and/or cytotoxic T lymphocyte epitopes, giving a product which causes

potent immune responses to the coupled peptide in members of

Stimulator consists of (A) a promiscuous helper T cell epitope (Th)

which elicits an immune response to the coupled peptide in members of

a heterogeneous population expressing diverse HLA phenotypes, and (B)

a adjuvant peptide sequence from the invasin protein of Yersinia.

Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten

components. When the hapten is LHRH, then optionally the invasin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                R82571-91 are helper T cell epitopes which can be used in the preparation of a peptide immunogen that is useful in vaccines for treating allergic reactions. In the immunogen an IgE CH4 peptide is attached C-terminally to a series of amino acids including a helper T cell epitope. The immunogen may also opt. contain a fatty acid derivative, an invasin domain or alpha-NH2. The immunogen produces high titres of antibodies to the effector site in human IgE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens may be used in either a radially branching multimeric form or a linearly arranged monomeric form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....blt mast
immunogens
                                                                           epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sal immune stimulator.
stimulator; invasin; hapten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                contg. IgE CH4 peptide and helper.ing antibody prodn. for allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                        cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 22;
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                                                                        H
                                                                      immunogen; helper
                                                                                       constant heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..0
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
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immune sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 152;
Pred. No. 2
0; Mismat
                             13-JUN-1996 (first entry)
Tetanus toxin helper T cell epitope, T'
IGE; CH4; immunoglobulin; epsilon; immunoglobulin; epsilon; immunoglobulin; epsilon; immunog526365-A1.
WO9526365-A1.
05-OCT-1995; U03741.
28-MAR-1995; US-218461.
25-OCT-1994; US-218461.
25-OCT-1994; US-328912.
(UNBI-) UNITED BIOMEDICAL INC.
Wang CY;
WPI; 95-351297/45.
Synthetic peptide-based immunogen contgressions.
                                                                                                                                                                                                                                                              immunogen cont
for eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; tetanus toxin.
Clostridium tetani.
W09425060-A.
10-NOV-1994.
28-APR-1994; U04832.
27-APR-1994; US-057166.
14-APR-1994; US-229275.
(LADD/) LADD A E.
(WANG/) WANG C Y.
(ZAMB/) ZAMB T.
Ladd AE, Wang CY, Zamb T;
WPI; 94-357910/44.
Immunogenic luteinising hormone rethants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for use in universal
    AA.
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Best Local Similarity 100.0%;
Matches 20; Conservative
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standard; peptide;
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R62693;
10-SEP-1995
Helper T cel
Helper T cel
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Peptide immunogen useful in treatment of allergy - comprises

membrane-bound IgE epsilon-chain peptide synthesised linearly in

tandem with T helper epitope peptide

Claim 2; Page 18; 53pp; English.

W05957-W05616 represent helper T cell epitopes used in the peptide

immunogens of the invention. This sequence represents the tetanus toxin

helper T cell antigen. The peptides of the invention contain one of

these sequences, and a membrane-bound immunoglobulin E (IgE) fragment

(see W05595 and W05596). The peptide immunogens of the invention can be

used in vaccines for the immunotherapeutic treatment of allergenic

reactions, including allergic rihinitis, food allergies, anaphylaxis,

reactions, including allergic rihinitis, food allergies, anaphylaxis,

reactions, including allergic rihinitis, food allergies, anaphylaxis,

virally-induced asthma. The immunogens overcome the short effective

period of antihistamines, decongestants, and beta-2 agonists, while

preventing the broad immunosuppression of corticosteroids. The peptides

do not have the potential side effects of restlessness or sedation

(associated with antihistamines), associated increased morbidity in

sechnatics (as seen with beta-2 agonists) and adverse hormonal activities

(beginned of an activities and astroned activities)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activities
                                                                                                                                                                                                                                                                  10-DEC-1996 (first entry)

Tetanus toxin helper T cell epitope #2.

Immunoglobulin; IgE; membrane protein; human; epsilon chain; hepatitis B membrane anchoring domain; helper T cell; surface antigen; core antigen; pertussis toxin; tetanus toxin; measles virus F protein; immunotherapy; chlamydia trachomatis major outer membrane protein; immunogen; vaccine; chlamydia trachomatis major outer in the special circumsporozoite; E. coli TraT; schistosoma mansoni; triose phosphate isomerase; allergenic reaction; allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma; antihistamine; decongestant; beta-2 agonist; immunosuppression;
                                                                                                                 0;
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                      epitope
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  stimulator component.
a tetanus toxin helper
immune stimulator.
                                                                                 Length
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region contg. peptide immunogen for treating
i; immunoglobulin; epsilon; immunogen; helper
allergy; antibody; constant heavy chain.
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08,
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Pred. No. 2.09e-08
0; Mismatches (
                                                                                DB 13
2.09e-(
                                                                                                              Mismatches
                                                                               152;
No.
                                                                             Score
Pred.
0; M
  the immune surpresents and Th in the in
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
W09612740-A1.
02-MAY-1996.
25-OCT-1995; U13841.
25-OCT-1994; US-328519.
(UNBI-) UNITED BIOMEDICAL INC.
Walfield AM, Wang CY;
WPI; 96-230555/23.
Peptide immunogen useful in trea membrane-bound IgE epsilon-chain
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D W05600 standa
C W05600;
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E Tetanus toxir
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WPH: 95-351297/45.

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WPH: 95-351297/45.

Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper

T cell epitope - useful for eliciting antibody prodn. for allergy

T cell epitope - useful for eliciting antibody prodn. for allergy

T cell epitope - useful for eliciting antibody prodn. for allergy

K82592-R82600 and R83560-R83581 are peptide immunogens that are

USECH4 peptide is attached C-terminally to a series of amino acids including a helper I cell epitope. The immunogen may also opt. contain a fatty acid or fatty acid derivative, an invasin domain or alpha-NH2.

CC in human IgE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens

CC in human lgE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens

CC may be used in either a radially branching multimeric form or a linearly arranged monomeric form.

SQ Sequence 32 AA;

"T cell peptide and helper on the immunogens of linearly arranged monomeric form.

"The Immunogen produces in either a radially branching multimeric form or a linearly arranged monomeric form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang CY;
Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper
T cell epitope - useful for eliciting antibody prodn. for allergy
T reatment
T cell epitope - useful for eliciting antibody prodn. for allergy
T reatment
S Claim 5; Page 69; 87pp; English.
S R82592-R82600 and R83560-R83581 are peptide immunogens; In the immunogens,
C useful in vaccines for treating allergic reactions. In the immunogens,
C useful in vaccines for treating allergic reactions. In the immunogens
C an IGE CH4 peptide is attached C-terminally to a series of amino acids
C including a helper T cell epitope. The immunogen may also opt. contain
C a fatty acid or fatty acid derivative, an invasin domain or alpha-NH2.
C The immunogen produces high titres of antibodies to the effector site
C The immunogen produces high titres of antibodies to the effector site
C The immunogen produces allergen-induced IgE prodn. The immunogens
C may be used in either a radially branching multimeric form or a
C linearly arranged monomeric form.
C Sequence 34 AA;
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Pred. No. 2.09e-08;
0; Mismatches 0;
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Pred. No. 2.09e-08
0; Mismatches
WO9526365-A1.
05-OCT-1995.
24-MAR-1995; U03741.
28-MAR-1994; US-218461.
25-OCT-1994; US-328912.
(UNBI-) UNITED BIOMEDICAL INC.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

search, using Smith-Waterman algorithm - protein database protein MPsrch_pp

MasPar time 4.52 Seconds 132.990 Million cell updates/sec Tue Aug 17 15:47:39 1999; Run on:

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>US-09-049-847-1 (1-15) from US09049847.pep 104 1 QYIKANSKFIGITEL 15 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 15

Scoring table:

40068593 residues 122810 seqs, Searched:

Post-processing: Minimum Match 0% Listing first 45

summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

scale 0.713 Variance 37.227; Mean 26.532; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

cursor - Clostr 31-Mar-1988 #te	U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Weller, U.; Hudel, M.; Habermann, E.; Niemann, (1986) 5:2495-2502 s toxin: primary structure, expression in E. cology with botulinum toxins.	<pre>ferences MUID:87053814 A25689 cule_type DNA dues</pre>	cule_type DNA dues 1-1315 ##label FAI s-references GB:X06214; NID:g40773; FID:g40774 rimental_source strain CN3911 A25194 Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O. J. Bacteriol. (1986) 165:21-27 Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in Escherichia coli.	H Z40 HO G ··i
RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE	и Ч	#cross-references #accession A25 ##molecule_typ ##residues ##cross-refere REFERENCE A25 #authors Fai #journal Nuc #title The #cross-references #accession A25	##molecule_type DN ##residues 1- ##cross-references ##experimental_sou REFERENCE A25194 #authors Fairwea #journal J. Bact #title Cloning	#cross-references MUI #accession A25194 ##molecule_type DN ##residues 74 #accession B25194 ##molecule_type pr ##residues 86 REFERENCE A60759 #authors Matsuda #journal Infect. #title Isolati

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2-31 ##label DEF

The source of this protein was an extrachromosomal plasmid.

The precursor is cleaved by endogenous proteinase activity to form light (fragment A) and heavy (fragment B.C) chains that are covalently linked by an interchain disulfide bond (the individua chains are not toxic when separated). The amino end of the heavy chain (fragment B) can be separated from the carboxyl end (fragment C) by papain.

Fragment B forms ion channels in a lipid bilayer. Fragment C binds to gangliosides and may target the toxin to the motor end plate.

Fragment A is a zinc-dependent endopeptidase.
    toxin
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de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonel
Montecucco, C.

Eur. J. Biochem. (1995) 229:61-69
Structural studies on the zinc-endopeptidase light
tetanus neurotoxin.
ces MUID:95262688
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#binding_site zinc (His) #status predicted\
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th 1315 #molecular-weight 150681 #checksu
  of
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                                                                                                                                                       tetanus
                                                                                                                                                                                                                                   Schiavo, G.; Benfenati, F.; Poulain, B.; Ros;
Laureto, P.P.; DasGupta, B.R.; Montecucco,
Nature (1992) 359:832-835
Tetanus and botulinum-B neurotoxins block ne
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  heavy
                                                                                               Demotz, S.; Lanzavecchia, L.; Eisel, Widmann, C.; Corradin, G. J. Immunol. (1989) 142:394-402
Delineation of several DR-restricted
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host Saimiri sciureus (common squirrel monkey)
16-Oct-1992 #sequence_revision 16-Oct-1992 #text
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ATP; P-loop; phosphotransferase
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                                                                              Ohkubo, S.; Muto, A.; Kawauchi, Y.;
Mol. Gen. Genet. (1987) 210:314-322
The ribosomal protein gene cluster
ces MUID:88142549
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1. No. 5.01e-01;
Mismatches 1
         KIYMC #type complete
adenylate kinase (EC 2.7.4.3) - Myc
#formal_name Mycoplasma capricolum
31-Dec-1990 #sequence_revision 31-r
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-references EMBL:X06414;
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hypothetical protein yeeB - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24-Sep-1998

E69792
A69580
Kunst, F.: Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, B.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,
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Shimpo,
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Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Xasuda, M.; Iabata, S.
DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
                                                                                                                                                                                                                                                                                                                                                                                   cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

accession S77138
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#length 284 #molecular-weight 31380 #checksum 3965
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e 63; DB 2; Len . No. 5.01e-01; Mismatches 3;
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8; Mismatches 2;
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25-Apr-1997 #sequence_revision
21-Aug-1998
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Score 63;
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C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Lauber, J.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.: Noback, M.; Noone, D.; O'Reilly, M.; Moestl, D.; Nakai, S.: Noback, M.; Noone, D.; O'Reilly, V.; Pohl, T.M.; Portetelle, D.; Porvolik, S.; Prescont, A.M.; Prescan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Schroeter, R.; Scrfone, F.; Sckiguchi, J.; Sakowska, A.; Takenaru, R.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Takenashi, H.; Takemaru, R.; Wedler, E.; Vassarotti, A.; Viari, A.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Vatawa, H.; Janaka, H.; Vannier, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Tawamoto, H.; Yamane, K.; Yata, Yata, Yata, Yata, Yata, Yata, Ya
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Whole-genome random sequencing and assembly of Haemophilus
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#formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
21-Nov-1998
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gene 84 protein - Mycobacterium phage L5
#formal_name Mycobacterium phage L5
30-Sep-1993 #sequence_revision 30-Sep-1993 #tex
09-Sep-1997
S31029
S30949
Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G
Mol. Microbiol. (1993) 7:407-417
Superinfection immunity of mycobacteriophage L5
for genetic transformation of mycobacteria.
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erences GB:Z46922; NID:g600818; PID:g600819
#superfamily gamma-glutamyltransferase
aminoacyltransferase; glycoprotein; heteroc
protein
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Cloning and expression of gamma-glutamyl isolated porcine brain capillaries.
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                                                                                                                                e 61; DB 2; L
. No. 1.19e+00;
Mismatches 3
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larity 53.3%;
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#formal_name Mus musculus #common_name house mous
19-May-1994 #sequence_revision 19-May-1994 #text_
17-Mar-1999
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EMBL:Z18946; NID:g15859;
nucleotide sequence was
library, December 1992
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#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08
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##residues 1-66
##cross-references E
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
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#length 287 #molecular-weight 32259 #checksum
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delta-endotoxin homolog yokG - Bacillus su
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997
24-Sep-1998
C69908
A69580
Kunst, F.; Ogasawara, N.; Moszer, I.; Albe
Alloni, G.; Azevedo, V.; Bertero, M.G.;
Bolotin, A.; Borchert, S.; Boriss, R.; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                       Score 59; DB 2; Le
Pred. No. 2.79e+00;
1; Mismatches 1;
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    ##residues
##cross-references GB:AE001566; GB
##experimental_source strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary
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larity 50.0%;
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#length 326
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M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haich, J.; Havond, C.R.; Henaut, A.; Hilbert, B.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Masuda, S.; Maueel, C.; Medina, N.; Mellado, R.P.; Mazuno, M.; Mosetl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.; Prescott, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, A.; Sato, T.; Schiguch, G.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Schiguch, J.; Schleich, S.; Schroeter, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tosato, V.; Uchiyama, S.; Schot, B.; Roche, P.; Tosano, M.; Vannier, F.; Vaslanck, A.; Tanako, H.; Vanane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.; Danchin, A.; Toshikawa, H.F.; Zumstein, E.; Vature, (1997) 390:249-256 The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
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type IIS restriction enzyme R protein - Hel
  (strain 26695)
#formal_name Helicobacter pylori
09-Aug-1997  #sequence_revision 09-Aug-1997
10-Oct-1997
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4.24e+00;
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   translation not sho
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##cross-references GB:Z99115; GB:PID:G2634580
##experimental_source strain 168
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35.7%;
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subunit C related protein - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
10-Oct-1997
B64382
A64300
Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton,
R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton,
R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
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#checksum 2148
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                                                                                    -423 ##label TOM

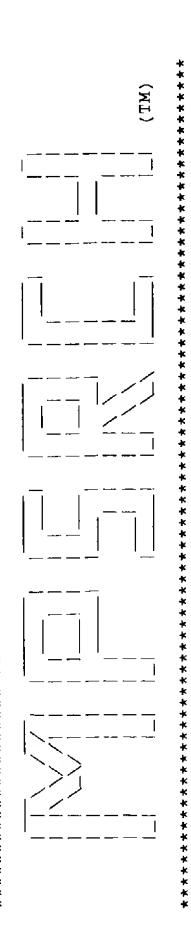
S GB:AE000637; GB:AE000511; NID:g2314536;

TIGR:HP1366

Th 423 #molecular-weight 50047 #checksum
                                                                                                                                                                                                                                                                                                     s73999 #type complete
hypothetical protein yaaC homolog VXpSPT7_orf;
pneumoniae (ATCC 29342) (SGC3)
hypothetical protein VXpSPT7_orf269
#formal_name Mycoplasma pneumoniae
ATCC 29342
27-Feb-1997 #sequence_revision 25-Apr-1997 #te
21-Aug-1998
S73999
S7399
S73327
Himmelreich, R.; Hilbert, H.; Plagens, H.; Pi:
B.C.; Herrmann, R.
Nucleic Acids Res. (1996) 24:4420-4449
Complete sequence analysis of the genome of tl
Mycoplasma pneumoniae.
rences MUID:97105885
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#superfamily conserved hypothetical r
#length 269 #molecular-weight 30435
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Pred. No. 6.40e+00;
4; Mismatches 5;
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#cross-references EMBL:AE000062; GB:U00089;
#note the nucleotide sequence was and the nucleotide sequence was a business.
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Helicobacter pylori
cross-references MUID:97394467
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larity 50.0%;
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##residues 1-25;
##cross-references El
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##residues 1-4
##cross-references
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Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.; Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
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                                                                                                                                          nucleic acid
n not shown
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##residues 1-322 ##label BUL
##cross-references GB:U67513; GB:L77117;
##cross-references TIGR:MJ0658; PID:g151
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No.
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TTG
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larity 61.5%;
Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

search, using Smith-Waterman algorithm protein database protein MPsrch_pp

MasPar time 3.28 Seconds 129.169 Million cell updates/sec Tue Aug 17 15:48:26 1999; Run on:

not generated. Tabular output >US-09-049-847-1 (1-15) from US09049847.pep 104 1 QYIKANSKFIGITEL 15 Title: Description: Perfect Score: Sequence:

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28268293 residues 77977 segs, Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

0.845 scale 32.173; Variance Mean 27.171; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

, SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure of the receptor binding fragment HC of tetanus neurotoxin.";

NAT. STRUCT. BIOL. 4:788-792(1997).

-!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77 BOND OF SYNAPTOBREVIN-2.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-|-PHE-77 SYNAPTOBREVIN.
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EMBL; M12739; G144921; -.

EMBL; X05214; G40774; -.

PIR; A25689; BTCLIN.

PDB; 1AF9; 29-APR-98.

PROSITE; PS00142; ZINC_PROTEASE; 1.

NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE; ZINC; PLASMID; INIT_MET 0 0 0 CHAIN 1 456 TETANUS TOXIN LICHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDG AND ARE NON-TOXIC AFTER SEPARATION.

THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO GANGLIOSIDE RECEPTORS SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                     surotoxins block neurotransmitter release
synaptobrevin.";
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BY SIMILARITY.
ZINC (CATALYTIC) (BY S
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C.;
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MEDLINE; 93010.
SCHIAVO G., POULAIN b.,
MONTECUCCO C.;
"Tetanus toxin is a zinc protein an
"Tetanus toxin is a zinc protee
IDENTIFICATION AS ZINC ...
MEDLINE; 93010948.
TING G., POULAIN B., ROSSETIO
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SCHIAVO G., BENFENATI F., P(DASGUPTA B.R., MONTECUCCO C"Tetanus and botulinum-B new Py proteolytic cleavage of NATURE 359:832-835(1992).
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MEDLINE; 97475217.
UMLAND T.C., WINGERT L.M.,
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SEQUENCE FROM N.A.
STRAIN=ATCC 27343 / KID;
MEDLINE; 88142549.
OHKUBO S., MUTO A., KAWAUCHI Y., YAMAO F., OSAWA S.;
I'the ribosomal protein gene cluster of Mycoplasma capricolu MOL. GEN. GENET. 210:314-322(1987).
-!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOF MAINTENANCE AND CELL GROWTH.
-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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ALBRECHT J.-C., NICHOLAS J.
NEWMAN C., WITTMANN S., CF.
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P10251;
01-MAR-1989 (REL. 10, C
01-MAR-1989 (REL. 10, L
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KANEKO I., SAIO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.

MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

MIYAJIMA N., HIROSAWA M., MURAKI A., NAKAZAKI N., NARUO K.,

HOSOUCHI I., MATSJNO A., MURAKI A., WADA I., WATANABE A.,

NAMADA M., YASUDA M., TABATA S.;

"Sequence analysis of the genome of the unicellular cyanobacteri
"Sequence analysis of the genome of the unicellular cyanobacteri
"Sequence analysis of the genome of the unicellular cyanobacteri
"Squechocystis sp. strain PCC6803. II. Sequence determination of
synechocystis sp. strain PCC6803. II. Sequence determination of
centire genome and assignment of potential protein-coding regions
DNA RES. 3:109-136(1996).

-!- CATALYTIC ACTIVITY: ATP + FMN = DIPHOSPHATE + FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKAMURA
                                                                                         geneti
                                                                 R.W.;
Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FAD
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                               GROUPS TOGETHER HSV-1
63, AND HCMV UL47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDYLTRANSFERASE; MULTIFUNCTIONAL ENZYME
                                                        rightmost 43 kbp c
conservation of g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBE_SYNY3 STANDARD; PRI; 284 AA.
P73651;
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN
ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE)
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                       Length 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIS SP. (STRAIN PCC 6803).
CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
   епоше
                                                              NICHOLAS J., CAMERON K.R., COLEMAN H., NEWMAN C.,
"Analysis of nucleotide sequence of the rightmost
herpesvirus saimiri (HVS) L-DNA: general conservat
organization between HVS and Epstein-Barr virus.";
VIROLOGY 188:296-310(1992).
-! SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGE
EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCN
                                                                                                                                                                                                                                                                                                                                                      e 63; DB 1; Len-
1. No. 8.08e-02;
Mismatches 3;
                                                                                                                                                                                                                                                                                                                               C2D70154 CRC32;
  saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as lo modified and this statement is not remorentities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                        Score 63;
Pred. No.
structure of the herpesvirus 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                               103350
                                                                                                                                                                                                                                                                                                                                                      Similarity 50.0%; 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                          ; G60384; -
; G330992;
G36812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G1652777
                                                                                                                                                                                                                                                                                                                                                                                                        QYITSNATFIGLSE
||| :|: | 1::|
QYIKANSKFIGITE
                                                                                                                                                                                                                                                                                                                                 AA;
                                        FROM N.A. 92230228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIBF OR SLÄ1882.
SYNECHOCYSTIS SP
                                                                                                                                                                                                                                                                                          480*
36812; Gsc.
ASSEMBLY.
B99 F
                                                                                                                                                                                                                                                                          EMBL; X64346;
EMBL; M86409;
PIR; G36812; G
CAPSID ASSEMBL
SEQUENCE 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFERASE;
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                                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA;
[1]
SEQUENCE F
  imary s
VIROL.
                                        SEQUENCE
MEDLINE;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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Matches
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                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RD / KW20;
MEDLINE; 95350630.
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.E KELESCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.D. KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.D. MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C. FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)
ACPD OR HI1366.
HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                  Indels
                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BANK
                                      e 62; DB 1; Len Nc. 1.34e-01; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o£
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e 61; DB 1; L
1. No. 2.20e-01;
Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B4D866EF CRC32;
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 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uenzae Rd.";
ince 269:496-512(1995).
FUNCTION: CONVERTS HOLO-ACP TO APO-ACP
THE PHOSPHOPANTETHEINE RESIDUE FROM ACE
FUNCTION IS NOT CLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568
 A4BFCA0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61;
Pred. No.
                                     62;
No.
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                                        Score
Pred.
8; M
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31380 MW;
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                                      Similarity 33.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANDLER M.S., SMITH R.A.;
SUBMITTED (FEB-1995) TO EM
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                             262
                                                                                                                                                                                                                                                           STANDARD;
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U32816; G1574198;
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| VIKANSKFIGITEL
                                                                                                                                                  ovikanskfigitel
                                                                                                                               HYLRPETKFAGLDQL
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Loutstation -
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                                                                                                                  TISSUE=BRAIN;

MEDLINE; 89377838.

A PAPANDRIKOPOULOU A., FREY A., GASSEN H.G.;

MEDLINE; 89377838.

T.Cloning and expression of gamma-glutamyl transpeptidase from isolated porcine brain capillaries.";

EUR. J. BIOCHEM. 183:693-698(1989).

C -!- CATALYTIC ACTIVITY: (5-L-GLUTAMYL)-PEPTIDE + AN AMINO ACID = PEPTIDE + 5-L-GLUTAMYL-AMINO ACID.

PEPTIDE + 5-L-GLUTAMYL-AMINO ACID.

-!- PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.

C -!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.

C -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

C -!- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercientiles requires a license agreement (See http://www.isb-sib.ch/announg or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOPROTEIN; TRANSMEMBRANE;
                                                                                  MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                            (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2)
GLUTAMYLTRANSFERASE) (GGT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·~ 10
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-01
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.. 28, LAST SEQUENCE UPDATE)
.. 28, LAST ANNOTATION UPDATE)
(GP84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 60; DB 1;
. No. 3.61e-
Mismatches
                                                                              VERTEBRATA;
A; SUIDAE; SU
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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Pred.
3; 1
                                                                             CHORDATA; VE
RMES; SUINA;
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:y 42.98;
servative
                                                               SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORI
ARTIODACTYLA; SUIFORMES;
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453
94
119
220
296
336
342
510
513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VG84_BPML5 STAN
Q05301;
01-FEB-1994 (REL. 2
01-FEB-1994 (REL. 2
01-FEB-1994 (REL. 2
GENE 84 PROTEIN (GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conser
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                                                                                                               N.A
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SEQUENCE
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CARBOHYD
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SEQUENCE
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Best Local S
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Matches
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                     HERETER WANNARA COCCOCCOCCOCCOCCA AND DDD COCCOCCOCCOCCA FEETER FEETER WANNARA WANNARA FEETER FEETER FEETER SO
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AS (BY SIMILARITY).
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                                                                                                   mycobacteriophage
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HUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TRNA PSEUDOURIDINE SYNTHASE) (URACIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquifex
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AUJAY M.,
                                                                                                                                                                                                                                                                                                                  66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.V.;
bacterium
                                                                                                                                                                                                                                                                                                                                               Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacteriu aeolicus.";
NATURE 392:353-358(1998).
-!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 5
ANTICODON STEM AND LOOP OF TRANSFER RNAS (EY SIMIL -!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE 5'-PHOSPHATE + H(2)0.
-!- SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOUR
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.Ω.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VE5;
MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W. GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., GRAHAM D.E., OVERBEEK R., OLSON G.J., SWANSON R.V.
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                                                                                                                                                                                                                                                                                                                     ; Le:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (
SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE S
HYDROLYASE).
                                                                                                expression genetics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32
                                                                                                                                                                                                                                                                                                                  e 59; DB 1;
No. 5.87e-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQUIFEX
                                                                                                                                                                                                                                                                                        CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
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                                                                                                                                                                                                                                                                                                                Score 59;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                        39F84CA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQUIFEX AEOLICUS.
BACTERIA; AQUIFICALES; AQUIFICACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                           "DNA sequence, structure and gene
a phage system for mycobacterial g
MOL. MICROBIOL. 7:395-405(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                       MM;
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70.0%;
rative
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A PROCESSING.
287 AA; 32259 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                        EMBL; Z18946; E1192416;
PIR; S31029; S31029.
SEQUENCE 66 AA; 7424
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sej
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                                                     FROM N.A.
93211282.
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84.
MYCOBACTERIOPHAGE
                                                                                                                                                                                                                                                                                                                             Similarity 7; Conse
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YIKANSKFIG
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;; TRNA PROC
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066922;
                                                     SEQUENCE
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Best Local S
Matches
                                                                 MEDLINE;
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LYASE;
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287

Length

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59;

Score

6.7%;

Match

Query

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UNCTION: REPAIR
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                                                                                                                                                                                                                                                          191
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PLASMODIUM
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ACT_SITE
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                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                          bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANURA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REICHENBERGER S., PFEIFFER P.; "Cloning, purification and characterization of DNA polymerase beta from Xenopus laevis -- studies on its potential role in DNA-end joining."; EUR. J. BIOCHEM. 251:81-90(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
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                                                                                                   (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
30FLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) /
3SFERASE (EC 2.7.7.2) (FAD PYROPHORYLASE)
                                                                                                                                                                                                                                                                          RES. 24:4420-4449(1996).
ACTIVITY: ATP + RIBOFLAVIN = ADP + FMN.
ACTIVITY: ATP + FMN = DIPHOSPHATE + FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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三
                                                                                                                                                                     MYCOPLASMA PNEUMONIAE.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; LL.
1.53e+00;
5;
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   · 노 ল
No. 5.87e-01
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000062; G1674379; -.
TRANSFERASE; NUCLEOTIDXLTRANSFERASE; MULTIFUN
SEQUENCE 269 AA; 30435 MW; 07AF8D7C CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEC-1998 (REL. 37, CREATED)
DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
POLYMERASE BETA (EC 2.7.7.7).
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No.
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Pred.
4; M
Pred
1;
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arity 80.0%;
Conservative
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ADENYLYLIRANSFERASE (EC
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QYIKANSKFIGITEL
                           \Omega
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EDLINE; 98151235.
                                                                                                                                                                                                                                                         sequence
                                            15
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 29342 MEDLINE; 97105885.
Similarity
                           27
                          pneumoniae.";
NUCLEIC ACIDS 1
-!- CATALYTIC 2
-!- CATALYTIC 2
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DPOB_XENLA

057383;

15-DEC-1998

15-DEC-1998

15-DEC-1998

15-DEC-1998
                                                                        RESULI 9
ID RIBF_MYCPN
AC P75587;
DT 01-NOV-1997
DT 01-NOV-1997
DT 01-NOV-1997
                                                                                                                                                  SYNTHETASE).
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Best Local
Local
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                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \ddot{\circ}
  SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
                                                                                                               ETA, GAMMA
REACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
DNA SYNTHES
PROCESSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIGENS)
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 K
KD AND 19 KD ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                               ALPHA, BE
DIFFERENT
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                                                                                                                                                                                                                                                                                                                                                                                                   REPLICATION
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"GAP-FILLING"
HER THAN IN A
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                                                                                                                                                                      FAMILY
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                                                        TRIPHOSPHATE
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the gene
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                                                                                         SUBUNIT: MONOMER.

IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05, CREATED)
33, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
PROTEIN 1 PRECURSOR (MEROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THAILAND).
HAEMOSPORIDA;
                                                                                                                                                                      TYPE-X
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1. No. 1.53e+00;
Mismatches 1;
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INVOLVED IN PRIMER
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INVOLVED IN PRIMER
(BY SIMILARITY).
6948CECC CRC32;
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  AIR POLYMERASE. CONDUCTS "GAE DISTRIBUTIVE FASHION RATHER
                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                         EMBL; Y15732; E1198727; -.
PROSITE; PS00522; DNA_POLYMERASE_X; 1.
TRANSFERASE; DNA-DIRECTED DNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, SEQUENCE FROM N.A.
PAN W., TOLLE R., BUJARD H.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ-!- SUBCELLULAR LOCATION: ATTACHED TO THE
CONDUCTS
                  IN A STEPWISE DISTRIBUTIVE FASHION RATEASHION AS FOR OTHER DNA POLYMERASES.

CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE
N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                      POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6948CECC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOLATE K1 , APICOMPLEXA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
7; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MACKAY M., GOMAN M., BONE N., HYI
STUNNENBERG H., BUJARD H.;
"Polymorphism of the precursor for Plasmodium falciparum merozoites EMBO J. 4:3823-3829(1985).
                                                                                                                                                                      TO DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 RJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38162
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                                                                                                                                                                    SIMILARITY: BELONGS
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38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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13-AUG-1987 (REL. C 01-FEB-1996 (REL. 3 01-OCT-1996 (REL. 3 MEROZOITE SURFACE F (PMMSA) (P190).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|:::||:|::||
IKANSKFIGITEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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s statement is not removed. Usage by and for commes a license agreement (See http://www.isb-sib.ch/annoto license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                    RIVEROS-MORENO, SCHWARZ R.T.,
                                                                                                                                                                                                                                                                                                                                                                   ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE OF 83 K
ANTIGENS
                                                           GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                          (ISOLATE WELLCOME).
APICOMPLEXA; HAEMOSPORIDA; PLÁSMODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS.

HOLDER A.A.;

SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPJ (POTENTIAL).

-!- PIM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF KD AND 19 KD ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIC KD AND 19 KD ANTIGENS WHICH ARE PLACE DURING SCHIZONT.

MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                       Length 1630;
                                                                                    74
                                                                                                                                                                                                                                                        Indels
                                                                                   PROTEIN
REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             major
                                                                                                                                                                                                                                                                                                                                                                                                                                   J.S.,
M.L.V.
                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE; 86014355.
HOLDER A.A., LOCKYER M.J., ODINK K.G., SANDHU J.S., NICHOLLS S.C., HILLMAN Y., DAVEY L.S., TIZARD M.L.V FREEMAN R.R.;
"Primary structure of the precursor to the three manantigens of Plasmodium falciparum merozoites.";
NATURE 317:270-273(1985).
[2]
                                                                                                                                                                                                                                       e 57; DB 1; Len . No. 1.53e+00; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                       05, CREATED)
33, LAST SEQUENCE UPDATE)
33, LAST ANNOTATION UPDATE)
PROTEIN 1 PRECURSOR (MEROZOITE
                                                           SIGNAL;
                                                                                                                                                                                                                     DD2F8628 CRC32
                                                                                   E SURFACE
DE SG(TP)
ANCHOR.
                                                                                                                                                                                                                                                                                                                          1639
                               EMBL; X03371; G929798; -.
PIR; A25120; SAZQK1.
PEAM; PF00008; EGF; 1.
MALARIA; MEROZOITE; POLYPROTEIN; REPEAT;
TRANSMEMBRANE; GPI-ANCHOR.
                                                                                           TRIPEPTIDE MEMBRANE AN
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111653
111653
1, 1872
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PLASMODIUM FALCIPARUM
EUKARYOTA; ALVEOLATA;
                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                               MSP1_PLAFW STAN
P04933;
13-AUG-1987 (REL. C
01-FEB-1996 (REL. 3
01-FEB-1996 (REL. 3
MEROZOITE SURFACE H
(PMMSA) (P195).
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IKANSKFIGITEL
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and this
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modified entities
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                                                               GLYCOPROTEIN;
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Z80835; E269877; -.
Z99112; E1185258; -.
LIST; BG11495; RIBC.
FERASE; NUCLEOTIDYLTRANSFERASE; MULTIFUNCTIONAL ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
C 2.7.1.26) (FLAVOKINASE) / FMN
(EC 2.7.7.2) (FAD PYROPHOSPHORYLASE)
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COQUARD D., HUECAS M., OIT M., VAN DIJL J., VAN LOON PSUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP + RIBOFLAVIN = ADP + FMN.
-!- CATALYTIC ACTIVITY: ATP + FMN = DIPHOSPHATE + FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.A
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                                                               SIGNAL;
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1.53e+00;
                                                                                                  SURFACE
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM
BACILLUS.
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license@isb-sib.ch)
                                                               REPEAT
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MEROZOITE; POLYPROTEIN;
3RANE; GPI-ANCHOP
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larity 46.2%;
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ID RIBC_BACSU STANDARD

AC P54575; P70987;

DT 01-OCT-1996 (REL. 34, C)

DT 01-NOV-1997 (REL. 35, Li

DE RIBOFLAVIN KINASE (EC 2

DE ADENYLYRANSFERASE (EC 2

DE SYNTHETASE).
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STRAIN#168;
GUSAROV I.V., YOMANTAS
PERUMOV D.A.;
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                     , G9865;
A24594.
8; EGF; 1
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                    ; X02919; G
A24594; A2
; PF00008;
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TRANSMEMBRANE;
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SUBTILIST; BG
TRANSFERASE;
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EMBL;
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an oligopeptidase
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE
LACTOCOCCUS.
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STRAIN=NCDO 763;

MEDLINE; 95096044.

MONNET V., NARDI M., CHOPIN A., CHOPIN M.C., GRIPON J.C.;

"Biochemical and genetic characterization of PepF, an oli
from Lactococcus lactis.";

J. BIOL. CHEM. 269:32070-32076(1994).

J. BIOL. CHEM. 269:32070-32076(1994).

-!- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AN
ACIDS WITH A RATHER WIDE SPECIFICITY.

-!- COFACTOR: BINDS A ZINC ATOM (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC MET)
ALSO KNOWN AS THE THIMEI OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 601
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L; Z32522; G510140; -.

L; Z32522; G510140; -.

SITE; PS00142; ZINC_PRCTEASE; FALSE_...

)ROLASE; METALLOPROTEASE; ZINC.

fAL 387 288 388 BY SIMILARITY.

TTTE 388 388 BY SIMILARITY.

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Q23500;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROBABLE ACONITATE HYDRATASE, CYTOPLASMIC (EC 4.
LYASE) (ACONITASE).
ZK455.1.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABE
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Mismatches 4;
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                                                                                   e 56; DB 1; L
. No. 2.44e+00;
Mismatches 3
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'TIDASE F (EC 3.4.24.-).
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35719
                                                                                   Similarity 53.8% 7; Conservative
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HYDROLASE;
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|PS4124;
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CATALYTIC ACTIVITY: CITRATE = CIS-ACONITATE + H(2)0.

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
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  RHABDITIDAE;
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WORMPEP; ZK455.1; CE03812.
PROSITE; PS00450; ACONITASE_1; 1
PROSITE; PS01244; ACONITASE_2; 1
PFAM; PF00330; aconitase; 1.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Smith-Waterman algorithm using database search, protein protein MPsrch_pp

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>US-09-049-847-1 (1-15) from US09049847.pep 104 1 QYIKANSKFIGITER 15 Title: Description: Perfect Score:

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Scoring

residues 54579741 179066 segs, Searched

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Minimum Match 0% Listing first 45

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Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

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P78872
P78872;
01-MAY-1997 (TREMBLREL. 03, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
1 FISSION YEAST (FRAGMENT).
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCES.
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                                                                                                  YOSHIKAWA H., DANCHIN A.;
EMBL/GENBANK/DDBJ DATA BANKS
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HYPOTHETICAL PROTEIN (FRAGMENT).
PLASMODIUM FALCIPARUM.
EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLissequence from N.A.
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BORRISS R., SCHROETER R.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DA EMBL; Z99107; E1182657; -.
EMBL; AF012532; G2318062; -.
EMBL; AF012532; G2318062; -.
FOUTENCE 598 AA; 67963 MW; 4093FE95 CRC?
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MEDLINE; 98162722.
YOSHIOKA S., KATO K., NAKAI "Identification of open reacconas.";
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D89222; D1014580;
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EMBL; M69147; G951373;
HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       046869 PRELIMINARY; PRT; 131 AA.
046869;
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
MHC CLASS II BETA CHAIN (FRAGMENT).
ICTALURUS PUNCTATUS (CHANNEL CATFISH).
EUKARYOTA; METAZOA; CHONDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; SILURIFORMES; ICTALURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \cup
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   Gaps
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                                                                                                                                                                                                                                                                                              LASMODIUM
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                                                       Length
                                                                                                                                                                                                                                                                                               Сч
                                                                                                                                                                                                                                        SEQUENCE UPDATE)
ANNOTATION UPDAI
                                                                                                                                                                                                                                                                                                                                                                                                                         e 59; DB 5; Le
. No. 9.52e-01;
Mismatches 2;
                                                                                                                                                                                                                                                                                               HAEMOSPORIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 7; L. Pred. No. 1.53e+00; 4; Mismatches 4
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, Q25857;
2 Q25857;
3 Q25857;
3 O1-NOV-1996 (TREMBLR.)
DT 01-NOV-1996 (TREMBLREL.)
DT 01-NOV-1996 (TREMBLREL.)
DE PFG377.
OS PLASMODIUM FALCIPARUM.
OC EUKARYOTA; ALVEOLATA; APICOMPLEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
PA HANDMAN E., OSBORN A.H., SYMONS F., VAN DRIEL.
MOL. BIOCHEM. PARASITOL. 74:143-156(1995).
"%Li Lo4161; G309688; -..
"%Li Lo4161; G309688; -..
"%Li Lo4161; G309688; -..
"%Li Lo4161; G309688; -..
"%Li Lo41628; Pred. No. 9.52
"rity 46.28; Pred. No. 9.52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                    Score 59; DB 5;
Pred. No. 9.52e-
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
HOGAN R.J., ANTAO A., WILSON M.R., MILLER
WALDBIESER G., WOLTERS W., CHINCHAR V.G.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ
EMBL; AF044406; G2852410; -.
                           D27065DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87529F38
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                             MM;
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14740 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%;
larity 46.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5
                           \infty
                           26518
                                                    Similarity 46.2%; 6; Conservative
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QYIKANSKFIGITEL
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                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                              ::::| || |:|
IKANSKFIGITE
                                                                                                                 YVRGHSSFITISE
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RX MEDLINE; 98044033.

RA ALBERTINI A.M., ALLONI G.,

RA ALTEDON G., BESSIERE P., BOLDIN A., BOCHERT S.

RA BORRISS R., BOURSIER L., BRANS A., BERGHELL S.C., BRON S.,

RA GORRISS R., BOURSIER L., CANDWELL B., CANDRON V., CARIER N.M.,

RA CHOIS.K., COONIN J., CONNERLON I.F., COMMINGS N.J., DENTEL R.A.,

RA CHILL S., ETHINGTON J., FARRET C., EFRRARIE E., FOULGER D.,

RA CHILL S., GLASER P., GOFFEAU A., GOLIGHILY E.J., GRAND G.,

RA CHILL S., GLASER P., GOFFEAU A., GALIZZI A., GALIERON N.,

RA CHILL S., GLASER P., GOFFEAU A., GALIZZI A., GRALLEN A.,

RA CHILL S., GLASER P., GOFFEAU A., HARWOOD C.R., HERNOT A.,

RA JORIS B., KARAMATA D., KASHARA Y., KLAER BLANCHARD M., JONES L.,

A JORIS B., KARAMATA D., KASHARA Y., KLAER BLANCHARD M., TAND C.,

RA KORITA K., LEVINE A., LIN H., MASUDA S., MAUCH C., MEDIGE C.,

RA KORNIA Y., KOBTFER P., MIZUNO M., MOESTI D., NAKAI S., NOBCK M.,

RA DONE D., O'REILLY M., OGHWARA A., OUDGA B., PARK S.H.,

RESECAN E., PUJIC P., MIZUNO M., MOESTI D., NAKAI S., NALEY

RESECAN E., PUJIC P., PORPITELLE B., RAPOPORT G., REY M., REYNOLDS S.,

RECHOCHI J., SERONSKA A., SEROR S.J., SERROR P., SHIN B.S.,

SOROKIN A., TAACONI E., TAARAGI T., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., TAARAGI T., TARAHASHI H., TAKEMARU K.,

A TARECHIN A., WABUTT R., WEDLER E., WEDLER H., WEDLER P., WEDLER E., WEDLER E., WEDLER P., WEDLER P., YOSHIKAWA H., YOSHIKAWA H., YOSHIKAWA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                  BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOSHIKAWA H., DANCHIN A.;
EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOLDO B., HILBERT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAILED PHAGES;
                 SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e 58; DB 2; Les
No. 1.53e+00;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56ABC286 CRC32
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Pred. No.
7; Misma
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40742 MW;
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07,
07,
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DUESTERHOEFT 1
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larity 35.7%;
Conservative
               0.5
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NATURE 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUNST F., OGASAWARA N.,
SUBMITTED (NOV-1997) TO
EMBL; Z99115; E1183607;
SEQUENCE 357 AA; 4074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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(TREMBLREL.
(TREMBLREL.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \infty
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                                                                                                                                                            SUBTILIS.
FIRMICUIES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLQGGNNFIGVTQL
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XIKANSKFIGITEL
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5; Conser
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                                                                                                                                                                                                                                                                                                                  N.A
                                                                                                                                                                                                                                                                                                                  FROM
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KARAMATA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 7
064021
064021;
01-AUG-1998 (7
01-AUG-1998 (7
01-AUG-1998 (7
XOKG PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIOPHAGE
                                                                                      PROTEIN
1-JAN-1998
1-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
                                                                                                                                                            BACILLUS S
BACTERIA;
                                                                                                                                                                                                                                                                                                                                                 STRAIN=168
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→ Local
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Best Loc
Matches
                                                                                                                     YOKG
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           REPARTED OOC OOC COLL SELECTION 
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SIRAIN=26695;

MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,

TOMB J.-F., WHITE O., KERLAVAGE A.R., GILL S., DOUGHERTY B.P.

TOMB J.-F., WHITE O., KERLAVAGE A.R., GILL S., DOUGHERTY B.P.

A FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.P.

A NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,

LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,

A MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,

BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.

COTION M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN

HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,

"M.S., PENTER J.C.,"
                                                                                     Gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΣZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter
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SON J.D., KELLEY J.)
WATTHEY L., WALLI)
                                                                                                                                                                                                                                                                                                              GROUP
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MEROZOITES
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O
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                                                         357
                                                                                      Indels
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Q03999;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MEROZOITE SURFACE ANTIGEN PRECURSOR 1 (PMMSA) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indel
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Nature 1997 Sep
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ITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF NTHE MATURATION TAKE PLACE DURING SCHIZONT.
SUBCELLULAR LOCATION: COULD BE ATTACHED TO THE MEN
                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
     BANK
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LAST ANNOTATION UPDATE)
R PROTEIN (MBCIIR).
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PLASMODIUM FALCIPARUM.
EUKARYOIA; ALVEOLAIA; APICOMPLEXA; HAEMOSPORIDA;
                                                       e 58; DB 9; L
. No. 1.53e+00;
Mismatches 2
   DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e 58; DB 2; L
. No. 1.53e+00;
Mismatches 3
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SUBDIVISION;
                             56ABC286 CRC32
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    EMBL/GENBANK/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                            CREATED)
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                                                                                                                                                                                                                                                                             HP1366.
HELICOBACTER PYLORI (CAMPYLOBACTER BACTERIA; PROTEOBACTERIA; EPSILON (HELICOBACTER)
                                                        Score
Pred.
7; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of pylori[published erratum appears 25;389(6649):412].";
NATURE 388:539-547(1997).
EMBL; AE000637; G2314537; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                          MW;
                                                                                                                                                                             JLT 8 PRELIMINARY;
025919;
01-JAN-1998 (TREMBLREL. 05, C
01-JAN-1998 (TREMBLREL. 05, L
01-NOV-1998 (TREMBLREL. 08, L
TYPE IIS RESTRICTION ENZYME R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50047 MW;
                                                       Similarity 35.7%; 5; Conservative
 5-1997) TO EM
3; G3025485;
7 AA; 40742
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0.0%
tive
                                                                                                              178
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AL PROTEIN.
423 AA; 5
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YIKANSKFIGITEL
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XIKANSKFIGITEL
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BLACKMAN M.J., LIN
SUBMITIED (XXX-199
SUBMITTED (AUG-1
EMBL; AF020713;
SEQUENCE 357 A
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HYPOTHETICAL 1
                                                      Query Match
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Best Local
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Matches
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01, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
PROTEIN PRECURSOR (FRAGMENT)
                                                                                                                    d genetic a chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                     ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEMOSPORIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 57; DB 5; Le . No. 2.46e+00; Mismatches 2;
                        EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                    e 57; DB 2;
No. 2.46e+0
Mismatches
                                                                                                                                                                                                                                                                                                                                                . 01, CREATED)
. 01, LAST SEQUENCE UPI
. 09, LAST ANNOTATION U
E PROTEIN PRECURSOR (FF
                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPC [1]
SEQUENCE FROM N.A.
MEDLINE; 93295445.
JONGWUTIWES S., TANABE K., KANBARA H.; "Sequence conservation in the C-terminal parajor merozoite surface proteins (MSP1) of field isolates.";
MOL. BIOCHEM. PARASITOL. 59:95-100(1993).
EMBL; D13363; D1003128; -.
PFAM; PF00008; EGF; 1.
MEROZOITE; EGF-LIKE DOMAIN.
                                                                                                                    detailed
r A3(2) ch
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Pred. No.
6; Misma
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                                                                                               DENAPAITE
                                                                                         REDENBACH M., KIESER H.M., DENAPAIJ KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a det the 8 Mb Streptomyces coelicolor A3 MOL. MICROBIOL. 21:77-96(1996).
EMBL; ALO31350; E1316910; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 424 AA; 45064 MW; B4BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FALCIPARUM.
ALVEOLATA; APICOMPLEXA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KANBARA
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                     Score
Pred.
3; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE; 93295445.
JONGWUTIWES S., TANABE K.,
                                                                                                                                                                                                   Similarity 46.7%; 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 46.28; Conservative
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ID Q25966

AC Q25966;

DT 01-NOV-1996 (TREMBLREL. 0)

DT 01-NOV-1996 (TREMBLREL. 0)

DT 01-JAN-1999 (TREMBLREL. 0)

DT 01-JAN-1999 (TREMBLREL. 0)

DT MAJOR MEROZOITE SURFACE P
                                                                                                                                                                                                                                                                                                            DLT 12
Q25981
Q25981;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1999 (TREMBLREL. 0
01-JAN-1999 (TREMBLREL. 0
MAJOR MEROZOITE SURFACE P
                        B.G
TO I
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                          FALCIPARUM
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                        ., BARRELL (AUG-1998)
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TGILEL
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IKANSKFIGITEL
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 SEQUENCE FROM N.A STRAIN=A3(2); PARKHILL J., BARR
                                                        SEQUENCE FROM N.A STRAIN=A3(2); MEDLINE; 97000351
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QYIKANSKFI
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PLASMODIUM
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EUKARYOTA;
                                  SUBMITTED [3]
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Best Local S
Matches
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Best I
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RMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
LES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES
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                                   GLYCOPROTEIN;
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                                                                                 ANTIGEN.
ANTIGEN.
ANTIGEN.
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SEQUENCE FROM N.A.
CATHERINE SALLES, PHILIPPE VALENTI, ARETI DARLAMITSOU,
NADINE HENDERSON, LORNA CAMPBELL, DAVID GLOVER;
"Sequencing the distal x chromosome of Drosophila mela
"Sequencing the distal x chromosome of Drosophila mela
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                        Length
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                                                                     POTENTIAL.
83K MEROZOITE SURFACE A
42K MEROZOITE SURFACE A
19K MEROZOITE SURFACE A
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL. 08, CREATED)
(TREMBLREL. 08, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
, 45.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                      e 57; DB 5; Len . No. 2.45e+00; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
7
                                   SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 57; DB 5; L. No. 2.46e+00; Mismatches 4
                                                                                                                                                                                                                                                           SULT 10
077436
077436
077436;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDAT
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPD
EG:34F3.5
DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATA
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                                    REPEAT;
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Pred.
4; M
                                                                                                                                                         Φ
                                                                                                                                                       Score Pred. 6; 1
GPI-ANCHOR.

EMBL; M64681; G160539; -.

PFAM; PF00008; EGF; 1.

MALARIA; MEROZOITE; POLYPROTEIN;

TRANSMEMBRANE; GPI-ANCHOR.
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MW;
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24
400
286
400
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45824
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                                                                                                                                                      Similarity 46.2%; 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PE(2);
SEEGER K.J., HARRIS D.;
SUBMITTED (AUG-1998) TO
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
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YIKANSKFIGITEL
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IKANSKFIGITEL
                                                                                                                                                                                                     FKKNNNFVGIADL
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01-NOV-1998 (TREMI

01-NOV-1998 (TREMI

01-NOV-1998 (TREMI

HYPOTHETICAL 45.1

SC1E2.18.

SCIE2.18.

STREPTOMYCES COEL;

BACTERIA; FIRMICUT
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25
287
383
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PLASMODIUM FALCIPARUM.

EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.

[1]

SEQUENCE FROM N.A.

MEDLINE; 93295445.

JONGWUTIWES S., TANABE K., KANBARA H.;

"Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from tield isolates.";

MOL. BIOCHEM. PARASITOL. 59:95-100(1993).

EMBL; D13359; D1003124; -.

REMBL; D13359; D1003124; -.

MEROZOITE; EGF-LIKE DOMAIN.
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T 01-NOV-1996 (TREMBLREL. 01, CREATED)

T 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

T 01-NOV-1996 (TREMBLREL. 09, LAST ANNOTATION UPDATE)

MAJOR MENOZOITE SURFACE PROTEIN PRECURSOR (FRAGMENT).

N SP1.

PLASMODIUM FALCIPARUM.

C EUKARYOTA; ALVEOLATA; APICOMPLEXA; HAEMOSPORIDA; PLASMODIUM.

[1]

S EQUENCE FROM N.A.

MEDLINE; 93295445.

A ONGWUIIWES S., TANABE K., KANBARA H.;

S SEQUENCE CONSERVATION in the C-terminal part of the precursor major merozoite surface proteins (MSP1) of Plasmodium falciparu field isolates.";

MOL. BIOCHEM. PARASITOL. 59:95-100(1993).

R FMBL; D13361; D1003126; -.

PFAM; PF00008; EGF; 1.

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Unit.K. Research F. Collins, Biocomputing Research 1998 University of Edinburgh, U.on rights by Oxford Molecular Ltd 3.1A John F. (ht (c) 1993-19 Distribution Release 3. Copyright

algorithm Smith-Waterman using search, database protein in prote MPsrch_pp

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14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

0.348 scale 53.652; Variance 99, ₽ 7 Mean Statistics

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SUMMARIES

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ALIGNMENTS

W67578 standard; peptide; 15 AA.

W67578 standard; peptide; 15 AA.

W67578 standard; peptide #4 for chimeric fimbrin/I-cell epitope peptide.

T-cell epitope peptide #4 for chimeric fimbrin/I-cell epitope peptide.

T-cell epitope peptide #4 for chimeric fimbrin; T-cell epitope;

W chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;

W U55843464-A.

W U5584464-A.

W U5584666

W U5584464-A.

W U5584666

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W U5584464-A.

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1997 (first entry) toxoid universal Th epitope IT830 15 standard; Protein; RESULT 2 ID W11505 standa AC W11505; DT 24-SEP-1997 DE Tetanus toxo:

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C through a linker to a solid phase, forming a complex of (A)-solid phase.

C through a linker to a solid phase, forming a complex of (A)-solid phase.

C through a linker to a solid phase, forming a secondary a secondary structure in a benign buffer after liberation from the solid phase, and further the (A)-solid phase complex complex compress an immunogenic substance and/or an immune mediator coupled on (A). The present sequence and/or an immune mediator coupled on (A). The present invention of chemical derivatives, characterised by covalently attaching molecules at attachment points. Alternatively (A) is used as a scaffold-peptide for attachment points. Alternatively (A) is used as a scaffold-peptide for the incorporation into an Immunostimulating Complex (Iscom) resulting and (A)-iscom complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. (A) derivatised with one or more peptides having fibronectin-, laminin- or vitronectin-like binding activities can be used for the promotion of cell-attachment to place and for promotion of wound healing. Also a derivatised (A) can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                        Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection

Example 7; Fig 24; 115pp; English.

Synthetic DNA coding for the wild-type universal Th epitope from tetanus toxoid, designated TT830, was fused to the 3'-end of DNA encoding heavy chain sequences from the humanised anti-Fc gamma RI monoclonal antibody H22. The resulting fusion protein was shown to be significantly more efficient in antigen presentation and T cell stimulation that the TT830 epitope alone. A similar fusion construct was prepared coding for a mutant, antagonistic form of the epitope (designated TT833) fused to the anti-Fc gamma RI. The Fab22-TT833S is at least 100 times more effective than TT833S in funitioning T cell activation.
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19-DEC-1996.
07-JUN-1996; U09988.
07-JUN-1995; US-484172.
(MEDA-) MEDAREX INC.
Deo YM, Goldstein J,
WPI; 97-052242/05.
N-PSDB; T58127.
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for
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HER 2/neu; infecovarian cancer.
                                                                     such
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                        as a d:
detect
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Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - as universal carriers for prepn. of immunogenic conjugate(s) use as vaccines.

Claim 1; Page 17; 20pp; English.

Epitopic peptides may be used with synthetic hapten derived a pathogen to generate an immune response to the pathogen.

Peptides are recognised by numerous T-helper cell clones with the context of a wide range of alleles of the human MHC.

The peptides may be used in an antimalarial vaccine inducing
                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               histocompatibility complex;
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N US5837243-A.
17-NOV-1998.
07-JUN-1996; 661052.
07-JUN-1996; US-661052.
07-JUN-1995; US-484172.
NEDA-) MEDAREX INC.
Deo YM, Goldstein J, Graziano R, Somasundaram C; WPI; 99-023374/02.
Specific killing of tumour comprising an compressing an compression compressing an compression compress
                      aptamers
l be used
r of a dis
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. No. 4.95e-05;
Mismatches 0
                                                                                                                                                                                                        \sim \circ
                                                                                                                                                                         DB 27;
ection of specifically-binding aptadiagnostic-(A) molecules could be n or indicative of pregnancy or of autoimmune or cancerous disease.
                                                                                                                                                                      e 104; DB 2
No. 4.95e<sup>-</sup>
Mismatches
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Pred.
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                              AA
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EP-378881-A.

25-JUL-1990.

27-DEC-1989; 203318.

17-JAN-1989; IT-019110.

16-NOV-1989; IT-022409.

(ENIE ) ENIRICERCHE SPA.

Pessi A, Bianchi E, Verdini A

WPI; 90-225582/30.
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100.08;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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15 AA;
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W73220 standard; Protein W73220;
25-JAN-1999 (first entr Tetanus toxoid epitope. Multispecific single cha antibody-dependent celluantibody-dependent celluantibody-dependent celluantibody-dependent celluantibody-dependent
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15; Conser
                                                                                                                                                                                                   Similarity
15; Conser
                        selection
                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4

ID R06310 standard;
AC R06310;
DT 04-DEC-1990 (fi
DE Tetanus toxin ek

KW Tetanus toxin; v
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                                            agent. Such
derived from
infectious,
Sequence 1
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English

57pp;

4.6

27

Column

conjugate

peptide

carbohydrate tumour.

antibody;
; epitope;

carrier be

- comprises epitopes to

s vaccine multiple

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enabling nseq

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Tetanus toxin; vaccine; antibody dendrimeric poly-lysine; epitope Clostridium tetani.
W09843677-A1.
08-OCT-1998.
27-MAR-1998; E01922.
27-MAR-1997; US-041726.
(INSP) INST PASIEUR.
Bay S, Cantacuzene D, Leclerc C, WPI; 98-557071/47.
Carbohydrate peptide conjugate us with dendrimeric poly-lysine enak covalently attached Disclosure.

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                                               growt
                                                                                                                  infectio
This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal grow factor receptor (EGFR), comprises contacting the tumour cell with a multispecific protein molecule (preferably a single chain antibody) comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to treating cancers especially breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infecti by a target cell.
                                  cell
                                                                                    a portion w
s especially
                                                                                                          also
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                            26-NOV-1998 (first entry)
Universal helper T-cell epitope P2 derived from tetanus toxin.
Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3; hepatic and erythrocytic stage protein; PyHEP17; vaccine; malaria parasite; teanus toxin; P2; helper T-cell epitope.
                                                                                                                                                                               ;
0
                                                                                                                                                                               Indels
                                                                                                                                                       Score 104; DB 37;
Pred. No. 4.95e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                            15
                                                                                                                                                       100.0%;
Similarity 100.0%;
15; Conservative
                                                                                                                                                                                                                                                           standard; peptide;
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W71321 stand
W71321;
26-NOV~1998
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Sequence
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Matches
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int (residues
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                                                                                                         standard; peptide;
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| fragment
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toxin

LT 7 W67033 stand W67033; 15-DEC-1998 Tetanus toxi

AC AC DE

RESULT

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Disclosure, Page 13; 55pp; English.

Disclosure, Page 13; 55pp; English.

The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an antibody purified from biological fluid or cells of organisms administered with the carbohydrate peptide conjugate, and (2) a diagnosis kit comprising antigen-specific antibodies elicited by immunisation with the carbohydrate peptide conjugate. The peptide conjugate, antibody and diagnosis kit are used to provide pharmaceutical compositions and ciagnosis kit are used to provide pharmaceutical compositions and against viral infections caused by hepatitis virus, HIV or cytomegalo virus. They can be used to enhance immune responses, especially B- and T- cell responses, of humans and animals against bacterial infections. The carbohydrate peptide conjugate stimulates the antibody and T-cell is capable of increasing the survival of tumour bearing humans and animals. The present sequence corresponding to this sequence may be used to sa an epitope in a carbohydrate peptide conjugate. Sequence corresponding to this sequence may be used sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weylsbull-Al.

16-OCT-1997.

17-OCT-1997.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-000398.

18-OCT-1995; DEN-00398.

18-OCT-1997; DEN-00398.

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ID W35445 standard; peptide; 16 AA.

NC W35445;

NT 22-APR-1998 (first entry)

NE T-cell stimulatory peptide SEQ ID NO:51.

NW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumma scaffold; inhibition; metastasis; wound healing; solid phase.

NW W09738011-A1.

D 16-OCT-1997.

F 03-APR-1007 - 1
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Immunostim
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I. No. 4.95e-05;
Mismatches 0;
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Pred. No. 4
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Best Local Similarity 100.0%;
Matches 15; Conservative
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10-DEC-1996 (first entry)
Tetanus toxin helper I cell epitope #1.
Immunoglobulin; IgE; membrane protein; human; epsilon chain; hepatitis B
membrane anchoring domain; helper I cell; surface antigen; core antigen;
membrane anchoring domain; helper I cell; surface antigen; core antigen;
pertussis toxin; tetanus toxin; measles virus F protein; immunogen; vaccine;
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h inhibit mast
The immunogens
Complex (Iscom) resulting an (A)-Iscom complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. (A) derivatised with one or more peptides having fibronectin-, laminin- or vitronectin-like binding activities can be used for the promotion of cell-attachment to plastic surfaces, in particular to inhibit tumour growth and metastasis, and for promotion of wound healing. Also a derivatised (A) can be used for the selection of specifically-binding aptamers or as a diagnostic agent. Such diagnostic-(A) molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an infectious, autoimmune or cancerous disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetanus toxin helper T cell epitope, TTI.

Tetanus toxin helper T cell epitope, TTI.

Tetanus toxin helper T cell epitope, TTI.

Tetanus toxin helper T cell epitope; immunogen; helper T cell; epitope; clostridium tetani.

Mo9526355-AI.

MO952635-AI.

MO952635-AI.

MO952635-AI.

MO952635-AI.

MO952636-AI.

MONEL.

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Pred. No. 4.95e-05
0; Mismatches
                                                                                                                                                                                                                                                                                           DB 27;
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Mismatches
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0; Mismat
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15; Conservative
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15; Conservative
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R82573 standard; peptide;
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W05599;
10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R82573;
13-JUN-199
Tetanus to:
IgE; CH4;
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Best Local S
Matches
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Synthetic.

Wo9612740-A1.

D C2-MAY-1996.

25-OCT-1994; US-328519.

A Malfield AM, Wang CY;

Walfield AN, Wang CY;

Walfield AM, With antihistamines), and adverse hormonal activities

Commenced in corticosteroid users).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activities
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Nov425060-A.

Clostridium tetani.

Nov425060-A.

10-NoV-1994.

28-APR-1994; US-229275.

R (AADA) LADD A E.

(WANG/) WANG C Y.

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diphtheria toxin; plasmodium falciparum; circumsporozoite; E. coli Tischistosoma mansoni; triose phosphate isomerase; allergenic reaction; allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma; antihistamine; decongestant; beta-2 agonist; immunosuppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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. No. 4.95e-05;
Mismatches 0
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larity 100.0%;
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cell epitope;
tetanus toxin.
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R62692;
10-SEP-1995
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Helper T cel
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               domain
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                                                                                                                                                                                                                                                                                                                                      re peptide coil
                                                                                                                                                                                                                                                                                                                                 This T-cell antigen TT2 peptide may be attached to a core peptide contained in one of the 2 subunits of an alpha-helical coiled-coil heterodimer. Each core peptide is comprised of terminal and internal AA repeat sequences. This peptide antigen is attached to the core peptide through covalent linkages to certain AA of the internal repeats. The 2 subunits of the heterodimer are arranged in a stable alpha-helical coiled-coil configuration having a 1:1 stoichiometry, and the peptide antigen is disposed toward the oute surfaces of the configuration. The heterodimer may be used as a synthetic vaccine (optionally multivalent) or to generate
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                                                                                                                                                                                                                                                                                                 configuration
              invasin
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I cell; ep
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1; helper
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core peptide;
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                                                                  DB 13;
.95e-05;
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4.95e-05;
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                                        stimula
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JH4 region contg. peptide immunogen for t
CH4; immunoglobulin; epsilon; immunogen;
ine; allergy; antibody; constant heavy ch
                                                                Score 104; DB 1
Pred. No. 4.95e-
0; Mismatches
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         hapten is LHRH, then
the immune stimulator
represents a tetanus
                                                                                                                                                                                                                                                                                               immunogen in each sub:unit
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Pred. No. 4
0; Mismat
                                                                                                                                                                         first entry)
igen TT2 peptide.
vaccine; antibody; T-cell;
t; coiled-coil heterodimer;
                                       immune
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US-245507.
SYNTHETIC PEPTIDES INC.
Hodges RS, Houston ME,
                             represents
Th in the j
                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                           AA
                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R82596 standard; peptide; 27 AA R82596; 13-JUN-1996 (first entry) IGE CH4 region contg. peptide ige; CH4; immunoglobulin; epsil vaccine; allergy; antibody; con Synthetic. W09526365-A1. 05-OCT-1995. U03741. 28-MAR-1994; US-218461. 25-OCT-1994; US-328912. (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                        T-antigen; vaccine; antibody; alpha-helix; coiled-coil hete Synthetic.
W09531480-A1.
23-NOV-1995.
18-MAY-1994; US-245507.
(SPIS-) SPI SYNTHETIC PEPTIDE Cachia PJ, Hodges RS, Houst Zhou NE;
WPI; 96-010880/01.
Hetero:dimeric polypeptide in with different antigens on eafor antibody prodn.
Claim 7; Page 61; 95pp; Engli This T-cell antigen TT2 pepticontained in one of the 2 suk heterodimer. Each core pepti
                                                                                                                                                         standard; Peptide; 17
                                                                100.0%;
larity 100.0%;
Conservative
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100.0%;
rvative
           components. When the har
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15; Conservat
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                            The present sequence which can be used as
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                             Claim 5; Page 62; 87pp; English.

R82592-R82600 and R83560-R83581 are peptide immunogens that are useful in vaccines for treating allergic reactions. In the immunogens, an IgE CH4 peptide is attached C-terminally to a series of amino acids including a helper T cell epitope. The immunogen may also opt. contain a fatty acid or fatty acid derivative, an invasin domain or alpha-NH2. The immunogen produces high titres of antibodies to the effector site in human IgE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens may be used in either a radially branching multimeric form or a Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune
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WPI: 94-357910/44.

Immunogenic luteinising hormone releasing hormone peptide(s) -
that suppress LHRH activity in males and females

Claims 8, 12; Page 84; 213pp; English.

Synthetic immunogenic peptides are provided in which a universal immune

Synthetic immunogenic peptides are provided in which a universal immune

Claims 8, 12; Page 84; 213pp; English.

Synthetic immunogenic peptides are provided in which a universal immune

Claims 8, 12; Page 84; 213pp; English.

Synthetic immunogenic peptides are provided or protein. The

stimulator is linked to a peptide or protein. The

and/or cytotoxic T lymphocyte epitopes, giving a product which causes

potent immune responses to the coupled peptide or protein. The

stimulator consists of (A) a promiscuous helper T cell epitope (Th)

which elicits an immune response to the coupled peptide in members of

a heterogeneous population expressing diverse HLA phenotypes, and (B)

an adjuvant peptide sequence from the invasin protein of Yersinia.

Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the immune stimulator and hapten

can be omitted from the immune stimulator components. When the immune stimulator components.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
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       and helper r allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUTRH-containing immunogenic peptide.

LHRH-containing immunogenic peptide.

Helper T cell epitope; universal immune stimulator; invasin; havaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
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       H4 peptide produ. for
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  contg. IgE CF ing antibody
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4.95e-05;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            Score 104;
Pred. No. 4
  immunogen cont
for eliciting
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100.08;
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Synthetic peptide-based
T cell epitope - useful
treatment
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18..27
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US-057166.
US-229275.
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28-APR-1994; [27-APR-1993; [14-APR-1994; [CLADD/] LADD 7 (WANG/) WANG (
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R62701;
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13-JUN-1996 (first entry)

18-JUN-1996 (first entry)

18-JUN-1996 (first entry)

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Chin L;
WPI; 93-335491/42.

Induction of neutralising human monoclonal antibodies against human immuno:deficiences - by sepg. peripheral mono:nuclear cells human immunosideficiences - by sepg. peripheral mono:nuclear cells from blood using density gradient centrifugation, and treating cells by L-leucyl-L-leucine methyl ester etc.

Claim 1; ; 36pp; Taiwanese.

Claim 1; ; 36pp; Taiwanese.
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                                                  ·~ O
                               e 104; DB 13;
. No. 4.95e-05
. Mismatches
                               Score 104;
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0; Mismat
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                                 100.0%;
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rvative
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WANG/) WANG C Y.

A (ZAMB/) MANG C Y.

I Ladd AE, Wang CY, Zamb T;

R WPI; 94-357910/44.

I mmunogenic luteinising hormone releasing hormone peptide(s) -

T that suppress LHRH activity in males and females

Disclosure; Page 95; 213pp; English.

Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic I lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th)

which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse ELA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia.

Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.
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cell
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antibodies by in-vitro immunisation, which comprises: (a) separating peripheral mononuclear cells from blood using density gradient centrifugation; (b) treating the mononuclear cells with L-leucyl-L-leucine methyl ester; and (c) using the present antigen fragment, which is formed by coupled T and B cells, in a culture medium of human serum, IL-2 and T cells to effect cultivation and achieve in vitro immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                       hapten;
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immune stimulator;
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a hapten can be bonded
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                           R65383 standard; peptide; 37
R65383;
21-SEP-1995 (first entry)
Universal immunostimulator h
Helper T cell epitope; univertetanus toxin.
Synthetic.
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10-NOV-1994.
28-APR-1994;
27-APR-1993;
14-APR-1994;
(LADD/) LADD?
(WANG/) WANG
(ZAMB/) ZAMB
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                                                                                                                                                                                                                                                             Ladd AE, Wang CY, Zamb T;

Ladd AE, Wang CY, Zamb T;

Indunogenic luteinising hormone releasing hormone peptide(s) -

That suppress LHRH activity in males and females

Disclosure; Page 95; 213pp; English.

Synthetic immunogenic peptides are provided in which a universal immune

Stimulator is linked to a peptide or protein hapten containing B cell

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Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the

invasin and Th domains and between the immune stimulator and hapten

components. When the hapten is LHRH, then optionally the invasin domain

the present sequence is an example of a -GG-Th-GG-invasin immune

the present sequence is an example of a -GG-Th-GG-invasin immune
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ID R62723 standard; peptide; 47 AA.

AC R62723;

IT-SEP-1995 (first entry)

I IT-SEP-1995 (first entry)

W Helper T cell epitope; universal immune stimulator; invasin; hapten; w vaccine; LHRH; luteinising hormone releasing hormone; prostate; w tetanus toxin.

S Synthetic.

H Key
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universal immune stimulator;
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Pred. No. 4
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/note= "tetanus toxin
22..37
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                               tetanus toxin
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7-APR-1993;
1-APR-1994;
LADD/) LADD
VANG/) WANG
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10-NOV-1994.
28-APR-1994; U
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0-NOV-1994.
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Ladd AE,
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Immunogenic luteinising hormone releasing hormone peptide(s) -
That suppress LHRH activity in males and females
Claim 8; Page 88; 213pp; English.
Synthetic immunogenic peptides are provided in which a universal immune
stimulator is linked to a peptide or protein hapten containing B cell
and/or cytotoxic I lymphocyte epitopes, giving a product which causes
c stimulator consists of (A) a promiscuous helper T cell epitope (Th)
which elicits an immune response to the coupled peptide in members of
a heterogeneous population expressing diverse HLA phenotypes, and (B)
an adjuvant peptide sequence from the invasin protein of Yersinia.
Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the
invasin and Th domains and between the immune stimulator and hapten
components. When the hapten is LHRH, then optionally the invasin domain
can be omitted from the immune stimulator component.
The present sequence represents an LHRH-containing immunogenic peptide
as above which can be used as a potent vaccine for treating e.g.
                                                                                       immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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) generate vaccine to regulate CETP activity
)k of developing a cardiovascular disease e.
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"B-cell epitope comprises the C-ter
cids of human CETP, involved in
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Page 7; 72pp; English.
Ent vaccine comprises an immunogenic helper
tetanus toxoid protein covalently linked to
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W06131;
07-FEB-1997 (first entry)
Anti-cholesteryl ester transfer multivalent Cholesteryl ester transfer protein; CETP; an cardiovascular disease; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 4.95e-Mismatches
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Pred. No. 4.
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molecules"
2..15
/label= T-cell_epitope
/note= "T-cell epitope c
830-843 of tetanus toxoi
16..34
/label= B-cell_epitope
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Thomas LJ;
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Sequence 47 AA;
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Similarity 100.08;
15; Conserved:
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01-MAY-1996, U06147.
01-MAY-1995, US-432483.
(TCEL-) T CELL SCI INC.
Rittershaus CW, Thomas I
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decreasing the risk
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Cholesteryl ester
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vaccine
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epitopes of human cholesteryl ester transfer protein (CETP) (see also W06127). The vaccine elicits an immune response against endogenous CETP activity, and is used to treat or prevent a cardiovascular disease, such as atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 - or its fragments vaccine production.
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                                                                                                                                                                                      Score 104; DB 20; :
Pred. No. 4.95e-05;
0; Mismatches 0;
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P70345 standard; Protein; 573 AA.

AC P70345.

DT 22-APR-1991 (first entry)

DE Portion of B fragment and all of the C fragment

KW TT; Vaccine.

OS Clostridium tetani.

PN EP-209281-A.

PD 21-JAN-1986; 305029.

PR 28-JUN-1986; 305029.

PR 28-JUN-1985; GB-016442.

PR 28-JUN-1986; 305029.

PR 28-JUN-1986; 305
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                                                                                                           100.0%;
Similarity 100.0%;
15; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

using Smith-Waterman algorithm protein database search, protein MPsrch_pp

MasPar time 7.53 Seconds 100.464 Million cell updates/sec Tue Aug 17 16:07:31 1999; Run on:

not generated. output Tabular

>US-09-049-847-1 (1-15) from US09049847.pep 104 1 OYIKANSKFIGITEL 15 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

residues 50406085 seds, 411786 Searched:

Minimum Match 100% Listing first 1000 summaries Maximum DB seq length 15 Post-processing

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92 18:U93 19:NEWP 20:NEWU6 21:NEWU8 22:NEWU9

0.344 scale 56.870; Variance Mean 19.566; Statistics:

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. N score g and is

SUMMARIES

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red. M	2.56e-04 2.56e-04 2.56e-04 2.56e-04 2.56e-04 2.56e-04
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Description	Sequency Sequency Sequency Sequency Sequency Sequency Sequency
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DB	25 25 25 25 25 25 25 25 25 25 25 25 25 2
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Query Match 	0000000
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chosen parameters search due to from list summaries 993 Note: Post-processor removed

ALIGNMENTS

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         MOLECULE TYPE:
HYPOTHETICAL:
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US-08-716-249-4
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TYPE: a
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ID US-09-049-847
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Pred. No. 2.56e-04;
0; Mismatches 0;
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Pred. No. 2.56e-04
0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,889
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 69:
         09/046,37
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                                 Version
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CURRENT FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: US (
EARLIER FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Ve
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Stuart J.
: T-Cell E
S: 75
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St.
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1725 MW: 1
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STREET: 4560 Horton S
CITY: Emeryville
STATE: CA
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STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: Geysen, H.
APPLICANT: Rodda, Sturinte OF INVENTION: Trimber OF SEQUENCES:
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Local Similarity 100.0%;
nes 15; Conservative
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AA; 1725 MW;
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MOLECULE TYPE:
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INFORMATION F(
SEQUENCE CHI
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ORGANISM: C.
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                                        SEQ ID NO
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Briand, Jean-Paul
APPLICANT: Regenmortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies The
TITLE OF INVENTION: Uses Thereof for Vaccination
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

THE PC COMPUTER: DOS / MS - DOS / 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104;
Pred. No. 2.
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PRT;
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STREET: 1100 New York Avenue, S
CITY: Washington, D.C.
COUNTRY: USA
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CHARACTERISTICS:
1: 15 amino acids
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STANDARD;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,889A
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
                                                                         equence 69, Application US/08161889A
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
                                                                                                                                     STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
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                                    Sequence 1, Application US/09049847
GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Cantacuzene, Daniele
APPLICANT: Lo-Man, Richard
TITLE OF INVENTION: Mutiple antigen alycopeptide can
TITLE OF INVENTION: Comprising the same and use ther
FILE REFERENCE: 102.166A
CURRENT APPLICATION NUMBER: US/09/049,847
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/041,726
EARLIER FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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1. No. 2.56e-04;
Mismatches 0
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Pred. No. 2.56e-04
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GENERAL INFORMATION:
APPLICANT: Sudhir Paul
APPLICANT: Larry J. Smith
APPLICANT: Gennady Gololobov
TITLE OF INVENTION: Methods for Identify:
TITLE OF INVENTION: Inhibitors of Cataly!
TITLE OF INVENTION: Use
FILE REFERENCE: UNMC 63123
CURRENT APPLICATION NUMBER: US/09/046,37:
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3:0
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LENGTH: 15
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ORGANISM:
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                       Score 104; DB 5; Pred. No. 2.56e-04; 0; Mismatches 0
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1725 MW; 1
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larity 100.0%;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

using Smith-Waterman algorithm protein - protein database search, MPsrch_pp

MasPar time 1.99 Seconds 76.451 Million cell updates/sec Tue Aug 17 15:07:04 1999; Run on:

output not generated. Tabular

>US-09-049-847-1 (1-15) from US09049847.pep 104 1 QYIKANSKFIGITEL 15

Title: Description: Perfect Score: Sequence:

106580 seqs, 10152877 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

scale 0.346 Variance 50.688; Mean 17.539; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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lence 5, Applicationence 18, Applicationence 9, Applicationence 41, Applicationence 111, Applicationence 111, Applicationence 27, Applicationence 26, Applicationence 20, Applicationence		15 AA.		sion #1.30B
Sequences sequen	۲۸	PRT;	03	Dtd. Dtd. 0, Ver 1703 101
US-08-186 US-08-465 US-08-465 US-08-661 US-08-661 US-08-787 PCT-US92- PCT-US92- PCT-US92- PCT-US92- US-08-186 US-08-186 US-08-308 US-08-308 US-08-308 US-08-308 US-08-308 US-08-308 US-08-308	ALIGNMENTS	• • •	/TUS93117	topes Pty cell Epit Sell Epit Sell Epit St. St. St. St. St. St. St. St. St. St
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MOLECULE TYPE:
FRAGMENT TYPE:
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APPLICANT: Raumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
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1.64e-05;
                           Score 104; DB 3; L
Pred. No. 1.64e-05;
0; Mismatches 0;
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FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLFICK, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
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ZIP: 44114-2688

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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15; Conservative
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15; Conservative
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TOPOLOGY: linear
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ID US-08-661-
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Best Local
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Stashwant M. Dec.

Joel Goldstein:

Robert Graziano

Chezian Somasundaram

INVENTION:

THERAPEUTIC COMPOUNDS COMPRISED

TNVENTION:

OF ANTI-FC RECEPTOR ANTIBODIES

TNVENTION:

THERAPEUTIC COMPOUNDS

TNVENTION:

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Mismatches
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1995
                                                   Sequence 6, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPO
TITLE OF INVENTION: OF ANTI-FC RECEPT
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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Patent No. 5814617
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard C.
APPLICANT: Doolan, Denise L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 104;
Pred. No. 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/48
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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V: Synthetic IgE Membrane
V: Peptide Immunogens for
SS: 32
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Mismatches 0
        Stage
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   ХDа
                                                STALL
COUNTRY: U. 20889-5606
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMPUTER: IBM PC compatible
TYPE: SYSTEM: PC-DOS/MS-DOS
THE RELEASE #1.0, Ve
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                                                                                                   SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,704
FILING DATE: 07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                    equence 7, Application PC/TUS9513841
GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; W
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE M
TITLE OF INVENTION: Peptide Immunog
NUMBER OF SEQUENCES: 32
                                                                                                                                                      24,743
3R: 75,206
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Protective
Erythrocyti
11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DAIA:
APPLICATION NUMREP
                                                                                                                        FILING DATE: 07-OCT-1994
CLASSIFICATION: 424
AITORNEY/AGENT INFORMATION:
NAME: A. David Spevack
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,2
TELECOMMUNICATION INFORMATION:
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                        RESS:
1 Medical R
T-12, 8901
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AX: (301) 295-1022

DN FOR SEQ ID NO: 10:

E CHARACTERISTICS:

H: 15 amino acids
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                                                                                                                                                                                                                                                                                                                             STANDARD;
TITLE OF INVENTION: Pro
TITLE OF INVENTION: Ery
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medi
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                                   STREET:
CITY: Be
STATE: M
COUNTRY:
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ID PCI-US95-13841
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Mismatches 0
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and Treating Type I
23
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: and Treating Type
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                             -4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510
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08-JULY-1994
                                    APPLICATION NUMBER: 08/328,519
FILING DATE: 25-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-412
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                        104;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,2
FILING DATE: 08-JULY-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                               1619 CN;
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Pred.
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   25-0CI-1995
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SEQUENCE CHARACTERISTICS
LENGTH: 17 amino acids
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FILING DATE: 25-OCT-
CLASSIFICATION:
PRIOR APPLICATION DATA:
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3Y: linear
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Matches 15; Conser
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1981 MW: 1
                               : peptide
1981 MW; 1
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larity 100.0%;
Conservative
                                                     l 100.0%;
Similarity 100.0%;
15; Conservative
LENGTH: 1,
TYPE: amino acta
TOPOLOGY: linear
TOTUE TYPE: pept
        amino
o acid
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S-08-446-692-4
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and synthetic universal immune stimulators
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                                                                              Length 17
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                                                                        ; DB 3; Le
1.64e-05;
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                                                                             Score 104; DB 3
Pred. No. 1.64e-
0; Mismatches
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ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/446,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,323
ER: 1151-4146
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14-APR-1994
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FILING DATE: 27-APR-1992
CLASSIFICATION: 424
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         Application US/08488351A
                                                               CN
         23:
                                                                                                                                                                                                                                                                                                    Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
C.H. Lin
NUMBER: 29,3
                                                                                                                                                                                                                    Sequence 4, Application US/0848
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Xi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: and Syn
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                              1620
                                                                                                                                                                                                                                                                                                                                                                                                                           7-JUN-1995
N: 424
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 7-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-APR-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                         acids
                                                s: peptide
s: internal
1969 MW; 16
         V FOR SEQ ID NO:
CHARACTERISTICS
                                                                              Similarity 100.08
15; Conservative
                        amino
o acid
                                        inear
                                                                                                             17
                                                                                                            REGISTRATION
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                       LENGTH: 17 & TYPE: amino
                                               MOLECULE TYPE:
FRAGMENT TYPE:
SEQUENCE 17 AA;
                                                                                                                                                                                                                                                                                                                            Z
                                                                                                                                                           US-08-488-351A-4
                                       TOPOLOGY:
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SEQUENCE (
         INFORMATION
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                  SEQUENCE
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Best Local S
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and synthetic universal i
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.64e-05;
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                               DB 2;
1.64e-05;
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Pred. No. 1.64e-
0; Mismatches
                             ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                  17
                                             No. 1.64e Mismatches
                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: N. STATE: N. COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk

""" SYSTEM: PC-DOS/MS-DOS
""" SYSTEM: PC-DOS/MS-DOS
""" SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC COMPUTER: DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

TITMC DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic Li
TITLE OF INVENTION: and synthetic
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
                             104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1619 CN;
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 CN;
                             Score
Pred.
0; M
619
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vaccines
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            constructs immune stimulators
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                                                                                                                                           #1.25
                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995
          Immunogenic LHRH peptide
and synthetic universal i
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IR: 1151-4146
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27-APR-1992
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Epitopes
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Pred. No. 1
0; Mismat
                                                                                                                                                                                                   FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,2'
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,1'
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC/TUS9311703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9311703
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Grant Crant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stant D. Green f: 4560 Horton St. Emeryville
                                               Lin
        TITLE OF INVENTION: Immunog
TITLE OF INVENTION: and syr
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lir
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                        4134
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                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE: 7-JUN-1995
                                                                                                                                                                 FILING DATE: 7-JUN-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
ENCE 27 AA; 3165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%; 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 63, Application
GENERAL INFORMATION:
APPLICANT: Chiron Min
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                                                                                COUNTRY: ZIP: 101
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CITY: N
STATE:
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CITY: E
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), Timothy
:ON: Immunogenic LHRH peptide co
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:CES: 114
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Pred. No. 1.64e-
0; Mismatches
                                                                                                                                                                                                      STATE: ...

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VER
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146
TELECHONUNICATION INFORMATION:
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
LENGTH: 27 amino acids
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                                                                                   13, Application US/08445692
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                                                                   US/08446692
                                                                                                                                                                                                                                                                                                                                                                                                                                              CN;
                                                                                                                                                                              S: Maria C.H. Lin
345 Park Avenue
W York
                                                                                                                                                                                                                                                                                                                                                                                                                                              4134
             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang Y.
Timothy
                                                                                  Sequence 13, Application US
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang
APPLICANT: Zamb, Timoth
TITLE OF INVENTION: Imm
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   : peptide
3165 MW: A
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Wang, Chang
Zamb, Timot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application U
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang
APPLICANT: Zamb, Timot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
larity 100.0%;
Conservative
                                                                  Application
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15; Conser
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RESULT 9
ID US-08-446-692-13
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CIIY: N
STATE:
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JS-08-488-
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and synthetic universal 1
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APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351.
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                        REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57, Application US/08488351A
, 5843446
                                                                                                                                                                                                                                                  Score 104;
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14-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5843446

GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunog
TITLE OF INVENTION: and Syn
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: María C.H. Lin
                                                                                                                                                                                                                   8502
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O
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Maria C.H. L. 345 Park Avenue
New York
                                                                                                                                                                                                     peptide 4060 MW; 8
                                                                                                                                                                                                                                                100.0%;
Similarity 100.0%;
15; Conservative
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                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: SEQUENCE 37 AA;
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-08-488-351A-57
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CITY: Ne
STATE: N
COUNTRY:
ZIP: 101
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. No. 1.64e-05;
Mismatches 0
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                                               COMPUTER: IBM FC.
COMPUTER: IBM FC.
COMPUTER: Patentin Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
TENGTH: 31 amino acids
amino acid
single
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ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
  STALL
COUNTRY: CL.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COUNTRY: COUNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHI
TITLE OF INVENTION: and synthetic INUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
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3583 MW: F
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larity 100.0%;
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MOLECULE TYPE:
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Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
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1.64e-05;
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         Mismatches
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SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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Mismatches
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COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ER: 1151-4146
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APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
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FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,27
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
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Pred. No. 1
0; Mismat
                                                                                                                                         Application US/08488351A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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                                                                                 STANDARD;
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NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,
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4060 MW: 8
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       Conservative
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CITY: Ne
STATE: N
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and synthetic universal i
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FR: 1151-4146
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1151-4146
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                                                                                                                                                                                                                                                                                            Sequence 57, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHI
TITLE OF INVENTION: and synthetic NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                        Score 104;
Pred. No. 1
0; Mismat
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                                                                                                                                                                                                                                                                            US/08446692
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOSFRATING SYSTEM: US/08/446
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446
FILLING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/446
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                        CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C_{\mathbf{N}}
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TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACIERISTICS:
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NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                     STANDARD;
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                                                                                            : peptide 4060 MW: 7
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4060 MW: 7
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100.0%;
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Similarity 100.0%
15; Conservative
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TOPOLOGY: linear
MOLECULE TYPE:
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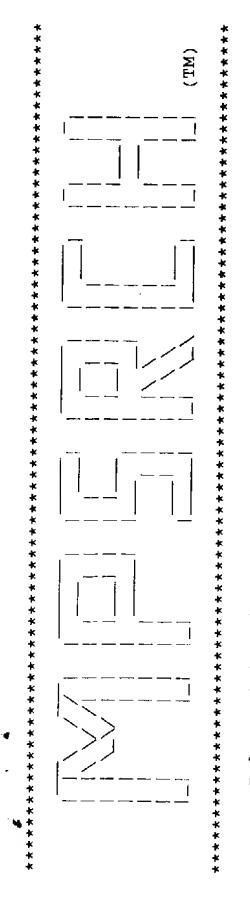
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Sequence 35, Application US/08446692
Patent No. 5759551
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LH
TITLE OF INVENTION: and synthetic
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                    US/08446692
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: peptide 7 AA; 5243 MW;
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Similarity 100.0%;
15; Conservative
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3Y: linear
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and synthetic universal i
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Pred. No. 1.64e-
0; Mismatches
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FR: 1151-4146
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
                                                                                                                                                                                                                                                                                                                                                                                                                        ,166
                                                                                                              Sequence 35, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRJ
TITLE OF INVENTION: and synthetic un
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,1
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                Application US/08488351A
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14-APR-1994
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
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                                                                                                                                                                                                        : Maria C.H. Lin
345 Park Avenue
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CITY: N
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ER: 1151-4146 US2
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No.
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STREET: 345
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOMPUTER: IBM PC compatible
TOMPUTER: 
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EILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

using Smith-Waterman algorithm - protein database search, protein MPsrch_pp

MasPar time 4.57 Seconds 184.098 Million cell updates/sec Run on:

Tue Aug 17 15:53:45 1999;

not generated. output Tabular

>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

40068593 residues 122810 seqs, Searched:

Post-processing

summaries 08 45 Minimum Match Listing first

Database:

4:pir4 pir60 1:pirl 2:pir2 3:pir3 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.604

48.854;

Variance

Mean 29.518;

Statistics:

	Pred. No.	11110	740-0	746-0	.82e-0	.82e-0	.82e-0	.82e-0	.82e-0	.15e-0	30e-0	30e-0	.30e-0	.30e-0	53e-0	.82e-0	.82e-0	.29e-0	.29e-0	296-0	.32e-0	340-0	34e-0	.34e
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SUMMARIES	ID	TCLT	3341	3979	4811	4810	4081	4063	4894	TCLA	4810	H025	H025	2117	I40645	MOAN	<u>M</u>	58	77	43	15	43	46	93
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ALIGNMENTS

BTCLIN #type complete tentoxylysin (EC 3.4.24.68) precursor - Clostridium tetani	recanus meurocoxin #formal_name Clostridium tetani 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 26-Feb-1999	A25689; A25757; A25194; B25194; A60759; S69348; S09364 A25689	<pre>Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.; Habermann, E.; Niemann, H.</pre>	EMBO J. (1986) 5:2495-2502 Tetanus toxin: primary structure, expression in E. coli, and	10:87053814		315 ##label EIS	ELETERICES GB:AU4436; NID:G40/69; PID:G40770 A25757	ner, N.F.; Lyness,	Acids Res. (1986) 14:7809-78	The complete nucleotide sequence of tetanus toxin.	757	_type_DNA	1315 ##labe	• •	##experimental_source strain CN3911 NCE A25194	athe	Thomson, R.O. Racteriol /log6, 166,01207	. bacceriot: (1980) 103:21 loning, nucleotide sequenc	oxin fragment C in Escherichia coli.	MOID. 6006 194	type DNA	3-1315 ##label FA2	erences GB:MJ B25194	_type protein R65-894 ##label pas	A60759	t, M.	ificat
RESULT 1 ENTRY TITLE ALTERNATE NAMES		ACCESSIONS REFERENCE	#authors	#Journal #title	#cross-refere	#accession ##molecule	##residues 1-13	**CLUSS TERENCE	NO.	#journal	#TITIE #CTOSS-TOFOTO	#accession	##molecule_	##residues	##cross-references	##experimer REFERENCE	#authors	#ionrnal	#title	t #OTOSS-Teferences	#accession	##molecule_	##residues ##Oxoogaan	##CIOSS-IEIELENCES #ACCESSION B25194	##molecule_ ##residues	REFERENCE	#authors #iournal	#title

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olecule_type protein
esidues
2-31 ##label DEF
The source of this protein was an extrachromosomal plasmid.
The source of this protein was an extrachromosomal plasmid.
The precursor is cleaved by endogenous proteinase activity to form light (fragment A) and heavy (fragment B.C) chains that are covalently linked by an interchain disulfide bond (the individual chains are not toxic when separated). The amino end of the heavy chain (fragment B) can be separated from the carboxyl end (fragment C) by papain.

Fragment C) by papain.
Fragment B forms ion channels in a lipid bilayer. Fragment C binds to gangliosides and may target the toxin to the motor end plate. Fragment A is a zinc-dependent endopeptidase.
This potent neurotoxin binds to peripheral neuronal synapses, is internalized, and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic cleavage of synaptobrevin (vesicle-associated membrane protein 2).
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    predicted #label TXC\
    #binding_site zinc (His) #status predicted\
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      heavy
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Delineation of several DR-restricted
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                                                                                                                                                                                                  rs Schiavo, G.; Benfenati, F.; Poulain,
Laureto, P.P.; DasGupta, B.R.; Mor
al Nature (1992) 359:832-835
Tetanus and botulinum-B neurotoxins
release by proteolytic cleavage of
references MUID:93063293
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   predicted #label TTL\
#product tentoxylysin heavy
   experimental #label TTH\
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de Filippis, V.; Vangelista, L
Montecucco, C.
Fur. J. Biochem. (1995) 229:61
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#label TXB\
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#fresidues 461-475
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s39791 #type complete
neurotoxin - Clostridium botulinum
#formal_name Clostridium botulinum
07-0ct-1994 #sequence_revision 01-Dec-1995 #text_change
24-Sep-1998
s39791
s39791
Campbell, K.; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta (1993) 1216:487-491
Nucleotide sequence of the gene coding for Clostridium
botulinum (Clostridium argentinense) type G neurotoxins
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                                                                 Collins, M.D.; Hutson, R.A.; East, A.K.; Al.
FEMS Microbiol. Lett. (1993) 108:175-182
Nucleotide sequence of the gene cocing for Cl
type F neurotoxin: comparison with other cl
neurotoxins.
ences MUID:93252228
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neurotoxin type F - Clostridium botulinum
#formal_name Clostridium botulinum
14-Jul-1995 #sequence_revision 10-Nov-1995
12-Jun-1998
                                        13-Jan-1995
               Clostridium
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S33411 #type complete
botulinum neurotoxin type F - Cl
#formal_name Clostridium barati
13-Jan-1995 #sequence_revision 1
08-Sep-1997
S33411; S31860
S33411
Thompson, D.E.; Hutson, R.A.; Ea
Collins, M.D.; Richardson, P.T
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Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. (1993) 31:2255-2262
Gene probes for identification of the botulinal neur
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neurotoxin type F - Clostridium botulinum
formal_name Clostridium botulinum
16-Aug-1996 #sequence_revision 16-Aug-1996 #
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East, A.K.; Richard...
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Roberts, I.A.; Ihompson, D.E.
FEMS Microbiol. Lett. (1992) 96:225-230
Sequence of the gene encoding type F new
Clostridium botulinum.
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##cross-references EMBL:X70820; NID:g407790;
##note the nucleotide sequence was s
Library, January 1993
EICATION #superfamily tetanus toxin
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Hutson, R.A.; Collins, M.D.; East, A.K.; Thompoolubel Hutson, R.A.; Collins, M.D.; East, A.K.; Thompoolubel Hutson, Nucleotide sequence of the gene coding for non-protective bridgium botulinum type B neurotoxin: comparison with other clostridial neurotoxins.
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##cross-references GB:M92906; NID:g144865; PID:g144867
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thors Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. (1993) 31:2255-2262
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##experimental_source non-proteolytic strain 2129B (Scott)
##note the nucleotide sequence was submitted to t
Library, January 1993
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##cross-references EMBL:X70819; NID:g407780; PID:g407781
##experimental_source non-proteolytic strain Eklund 2B (
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non-proteolytic botulinum neurotoxin type I
clostridium botulinum
#formal_name Clostridium botulinum
12-Aug-1996 #sequence_revision 12-Aug-1996
05-Jun-1998
140631; S48103; S48104; S36015
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TCATION #superfamily tetanus toxin
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#molecule_type DNA
#residues 634-1002 ##label CAM
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lin. Microbiol. (1993) 31:2255-2262
probes for identification of the botulinal n
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Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. (1992) 58:2345-2354
Molecular cloning of the Clostridium botulinum
gene encoding the type B neurotoxin and deter
its entire nucleotide sequence.
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#residues 36-217,'G',219-224,'S',226-246 ##label
#cross-references EMBL:Z11934; NID:g40383; PID:g40384
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thors Szabo, E.A.; Pombantal
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#residues 1-1291 ##label WHE
#cross-references GB:M81186; NID:g144734; PID:g144735
#experimental_source type B, Danish
#note sequence extracted from NCBI backbone
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GenBank entry CLOBOTB, release 103
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#formal_name Clostridium botulinum
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Biophys. (1985) 238:544-548
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                               Biol. Chem. (1992) 267:14721-14729
nimal essential domains specifying toxicity of the
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Poulain,
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#binding_site zinc (His
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Laureto, P.P.; DasGupta, I
Nature (1992) 359:832-835
Tetanus and botulinum-B neum
         ida, S.;
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#journal Biochem. Biophys. Res. Commun. (1989) 162:1388-1
#title Characterization of botulinum type A neurotoxin delineation of the N-terminal encoding region.
#accession A33401
                                                                                                                                                                                                                                                 al Niemann, H.

Niemann, H.

J. Biol. Chem. (1990) 265:9153-9158

The complete sequence of botulinum neurotoxin comparison with other clostridial neurotoxir sion A35294
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#cross-references EMBL:X52066; NID:g40381; PID:g4038
#experimental_source NCTC 2916
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FEBS Lett. (1995) 376:41-44
Molecular characterization of two forms o nontoxic-nonhemagglutinin components of botulinum type A progenitor toxins.
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idues 1-1296 ##label BIN

iss-references GB:M30196; NID:g144864; PID:g144

iss-references GB:M30196; NID:g144864; PID:g144

iss-references GB:M30196; NID:g144864; PID:g144

iss-references GB:M30196; NID:g144

issource strain 62A, subtype A

S09492

Thompson, D.E.; Brehm, J.K.; Oultram, J.

Shone, C.C.; Atkinson, T.; Melling, J.

Eur. J. Biochem. (1990) 189:73-81

The complete amino acid sequence of the type A neurotoxin, deduced by nucleoti
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J. Protein Chem. (1993) 12:351-363
Botulinum type A neurotoxin digested
97, 72, 45, 42, and 18 kD fragment
                                                                                                                                                        botulinum neurotoxin type A
#formal_name Clostridium botulinum
31-Mar-1993 #sequence_revision 31-1
15-May-1998
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  No. 8.82e Mismatches
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##residues 1-35 ##label BET
##cross-references GB:M27892; NID:g144880;
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Binz, T.
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neurotoxin type E - Clostridium botulinum (fragment;
#formal_name Clostridium botulinum
14-Jul-1995 #sequence_revision 10-Nov-1995 #text_cha
12-Jun-1998
S48106
S48106
S48103
Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. (1993) 31:2255-2262
Gene probes for identification of the botulinal neurogene and specific identification of neurotoxin type
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synaptosomal-associated 25K protein (SNAP-25)
#superfamily tetanus toxin
disulfide bond; hydrolase; metalloproteinase; ne
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#length 1296 #molecular-weight 149425 #checks
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cholinergic synapses. This toxin is activated by
two chains linked by a disulfide bond.
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Suedhof, T.C.; Jahn, R.; Niemann,
J. Biol. Chem. (1994) 269:1617-1620
Proteolysis of SNAP-25 by types E an
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1. No. 3.15e-04;
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#label LGHT\
#product bontoxilysin A heavy
#label HVY\
                                                      from NCBI
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                                                                                                #authors DasGupta, B.R.; Dekleva, M.L.
#journal Biochimie (1990) 72:661-664
#title Botulinum neurotoxin type A: se
   N-terminus and around the nic
#cross-references MUID:91120847
#accession A60025
##molecule_type protein
##residues 2-6;445-453,'X',455-457 ##
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##molecule_type process.
##residues 867-880;1148-1217,
##experimental_source strain Hall
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DasGupta, B.R.
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Biochem. Biophys. Res. Commun. (1992) 183:107-113
Sequences of the botulinal neurotoxin E derived from
Clostridium botulinum type E (strain Beluga) and
Clostridium butyricum (strains ATCC 43181 and ATCC
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botulinum neurotoxin type E precursor - Clo
(strain Beluga)
#formal_name Clostridium botulinum
30-Jun-1992 #sequence_revision 30-Jun-1992
08-Sep-1997
JH0257; B35294; A60027
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#authors Gimenez, J.A.; DasGupta, B.R.

#journal Biochimie (1990) 72:213-217

#title Botulinum neurotoxin type E fragmented wit 
Lys-C reveals the site trypsin nicks and 
tetanus neurotoxin.

#accession A60027
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3iol. Chem. (1990) 265:9153-9158
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omparison with other clostridial
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1. No. 7.30e-04;
Mismatches 0
                                   ##molecule_type DNA
##residues 1-367 ##label CAM
##cross-references EMBL:X70818; NID:g407784;
##note the nucleotide sequence was s
Library, January 1993
EICATION #superfamily tetanus toxin
neurotoxin
tDS #length 367 #checksum 184
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##residues 1-1251 ##label POU
##cross-references EMBL:X62089; NII
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thors Binz, T.; Kurazono, H.;
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##molecule_type DNA
##residues 1-1
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Biochem. Biophys. Res. Commun. (1992) 183:107-113
Sequences of the botulinal neurotoxin E derived from
Clostridium botulinum type E (strain Beluga) and
Clostridium butyricum (strains AICC 43181 and AICC
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#product botulinum neurotoxin heavy chain (t
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botulinum neurotoxin type E precursor - Clc
#formal_name Clostridium butyricum
30-Jun-1992 #sequence_revision 15-May-1998
15-May-1998
JH0256; S16145
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7; Mismatches
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Mismatches 0
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##experimental_source strains ATCC 43181
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#accession JHO
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#LICLE The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding gene.
#accession S21178
#moleculary
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botulinum neurotoxin type A - Clostridium botulinum
#formal_name Clostridium botulinum
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_ch?
16-Feb-1997
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Sequence of the gene coding for the neurotoxin of C.botulinum type A associated with infant botulism: comparison with other clostridial neurotoxins.
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J. Clin. Microbiol. (1993) 31:2255-2262
Gene probes for identification of the botulinal r
gene and specific identification of neurotoxin
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botulinum neurotoxin type E precursor - Clost #formal_name Clostridium botulinum
30-Sep-1993 #sequence_revision 30-Sep-1993 #t
12-Jun-1998
S21178; S48107; S18111
S21178
Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.;
Minton, N.P.
Eur. J. Biochem. (1992) 204:657-667
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f#residues 616-982 ##label CAM
f#cross-references EMBL:X70815; NID:g407786;
f#note the nucleotide sequence was the filter of the filter o
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##residues 1-1295 ##label RES
##cross-references EMBL:X73423; NID:g:
KEYWORDS neurotoxin
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#formal_name tomato spotted wilt virus
31-Mar-1993 #sequence_revision 31-Mar-1993
JQ0547
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     Length
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#journal J. Gen. Virol. (1990) 71:1001-1007
#title The S RNA segment of tomato spotted wilt ambisense character.
#cross-references MUID:90264829
#accession JQ0547
##molecule_type genomic RNA
##residues 1-464 ##label DEH
##cross-references DDBJ:D00645; NID:g222685; PID:d10
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 3.41 Seconds 173.887 Million cell updates/sec Tue Aug 17 15:54:28 1999; Run on:

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>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Title: Description: Perfect Score: Sequence:

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77977 seqs, 28268293 residues Searched:

Post-processing:

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Database:

swiss-prot37
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scale 0.675 Variance 44.662; Mean 30.150; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		H			SUMMARIES		
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                                                                                                                                                                                                                                                                                                                                                                                                                           Structure of the receptor binding fragment HC of tetanus
leurotoxin.";

NAT. STRUCT. BIOL. 4:788-792(1997).

NAT. STRUCT. BIOL. 4:788-792(1997).

-!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77

BOND OF SYNAPTOBREVIN-2.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-|-PHE-77 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboral between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announcersend an email to license@isb-sib.ch).
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EMBL; M12739; G144921; -.
EMBL; X06214; G40774; -.
PIR; A25689; BTCLTN.
PDB; 1AF9; 29-APR-98.
PROSITE; PS00142; ZINC_PROTEASE; 1.
NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE; 3D-STRUCTURE.
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AND ARE NON-TOXIC AFTER SEPARATION.
THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO G
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27
METALLOPROTEASE); ALSO KNOWN AS THE TETANUS,
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Pred. No. 2
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MEDLINE; 93063293.
SCRIAVO G., BENFENATI F., POULAIN B.,
DASGUPTA B.R., MONTECUCCO C.;
"Tetanus and botulinum-B neurotoxins b
                                                                                       "Tetanus toxin is a zinc protein and ineurotransmitter release and protease EMBO J. 11:3577-3583(1992).
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POULAIN B., ROSSETTO
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UMLAND T.C., WINGERT L.M.,
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IDENTIFICATION AS 3
MEDLINE; 93010948.
SCHIAVO G., POULAI)
MONIECUCCO C.;
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SEQUENCE FROM N.A.

SIRAIN-113 / 30;

MEDLINE; 94092745.

A CAMPBELL K., COLLINS M.D., EAST A.K.;

CAMPBELL K., COLLINS M.D., EAST A.K.;

TNUCLEOCTIC SEQUENCE Of the gene coding for Clostridium botulinum

(Clostridium argentinense) type G neurotoxin: genealogical comparison

with other clostridial neurotoxins.";

BIOCHIM. BIOPHYS. ACTA 1216:487-491(1993).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSIC

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND FRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPEPTIDASE.

-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A

ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE

CHANNEL FORMATION SECRETED (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM

NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM

NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

-!- SIMILARITY: BELONGS IF PREMEDATE THE MEDIATE THE
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G, HEAVY-CHAIN.
SIMILARITY).
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BOTULINUM NEUROTOXIN G
BOTULINUM NEUROTOXIN G
ZINC (CATALYTIC) (BY S
BY SIMILARITY.
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ZINC (CATALYTIC) (BY
INTERCHAIN (PROBABLE)
W; 8570B903 CRC32;
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No. 4.20e-
Mismatches
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LAST ANNOTATION UPDATI
TYPE G PRECURSOR (EC 3
                                                                                                        AA
                                                                                                                                                                                                                                             CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM
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Pred.
9; M
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larity 38.1%;
Conservative
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FNNFTVSFWLRVPKVSASHLE
                ITE; FOUNDS; Zn-procusing PO4958; 1AF9.
                                                                                                        STANDARD;
                                                                                                                                 CHEL. 35, C 01-NOV-1997 (REL. 35, L DI-NOV-1997 (REL. 35, L BOTULINUM NEUROTOXIN TY (BONTOXILYSIN G) BOTG.
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8; Conse
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01-NOV-1997
01-NOV-1997
01-NOV-1997
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CLOSTRIDIUM
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NEUROTOXIN;
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CLOBO
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SEQUENCE
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Similarity 21; Conser

Best Loc Matches

HYDROLASE

TRANSMEMBRANE;

NEUROTOXIN;

CHAIN

EMBL; S73676; G765179; -.
EMBL; X70820; G407791; -.
EMBL; X70816; G407789; -.
PROSITE; PS00142; ZINC_PROTEASE;
PFAM; PF00099; zn-protease; 1.
HSSP; P04958; 1AF9.

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The clink alternation of Substrate.

The control of Substrate and tetanus toxin.";

The control of the synaptobrevin/vamp family by types D and the control of the synaptobrevin.";

The control of Substrate and tetanus toxin.";

The control of Substrate and tetanus necessary to the control of Substrate and tetanus and teta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAST A.K., COLLINS M.D.; "Conserved structure of genes encoding components of botulinum "Conserved structure of genes encoding components of botulinum for the neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type F. CURR. MICROBIOL. 29:69-77(1994).
                                                                                                                                                                                                        BOTULINUM.
IRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 23387;
MEDLINE; 93012902.
EAST A.K., RICHARDSON P.T., ALLAWAY D., COLLINS M.D.,
ROBERTS T.A., THOMPSON D.E.;
"Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Φ
                                                                                                                                                 (BONT/F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 634-1002 FROM N.A.
MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.;
"Gene probes for identification of the botulinal neurotoxin specific identification of neurotoxin types B, E, and F.";
J. CLIN. MICROBIOL. 31:2255-2262(1993).
                                                                                                                                            .24.69)
                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
TYPE F PRECURSOR (EC 3.4
                                 AA
                             1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                               75:225-230(1992)
                        PRT;
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93 (REL. 26,
97 (REL. 35,
NEUROTOXIN T
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STRAIN=HOBBS FT10;
MEDLINE; 94297488.
                                                            01-JUL-1993 (REL. 01-JUL-1993 (REL. 01-JUL-1997 (REL. BOTULINUM NEUROTO (BONTOXILYSIN F).
                                                                                                                                                                        BOTE
CLOSTRIDIUM
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CLOSTRIDIUM.
                          CLOBO
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SEQUENCE
                                   P30996;
RESULT
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and
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                                                                                                           HYDROLASE; METALLOPROTEASE; ZINC.
BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN F, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
MW; 10954D22 CRC32;
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К.
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(EC 3.4.24.
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STRAIN=NCTC 7273;
MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.;
"Gene probes for identification of the botulinal specific identification of neurotoxin types B, E, J. CLIN. MICROBIOL. 31:2255-2262(1993).
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. No. 1.08e-05;
Mismatches 1
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DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ULULIUS (REL. 11, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
BOTULINUM NEUROTOXIN TYPE B PRECURSOR (EC 3 (BONTOXILYSIN B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS/CLOSTRIDIUM
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EMBL/GENBANK/DDBJ
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us toxin.
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SEQUENCE OF 1-16 AND 441-458. STRAIN=OKRA;
MEDLINE; 85197963.
SCHMIDT J.J., SATHYAMOORTHY V "Partial amino acid sequences E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35-245 FROM N.A.
7273;
PEMBERTON J.M.,
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                                                                                                                                                                                                                                    146709
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MEDLINE; 92384550.
WHELAN S.M., ELMORE M.J., B
MINTON N.P.;
                                                                                                                                                                                                                                                                      Similarity 57.1%; 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
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1274
227
228
231
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STRAIN=657;
MEDLINE; 89000987.
DASGUPTA B.R., DATTA A.
"Botulinum neurotoxin t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATTA A.
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IRMICUTES;
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P10844; P10843;
01-JUL-1989 (REL. 1
01-JUL-1993 (REL. 2
01-NOV-1997 (REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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STRAIN=NCTC 7273;
SZABO E.A., PEMBE
SUBMITTED (APR-19
                                                                                                                             encoding the ty
nucleotide sequ
APPL. ENVIRON.
[2]
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DISULFID
SEQUENCE
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Local S
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SEQUENCE
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METAL
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                                                                                                      MEDLINE; 93063293.

MEDLINE; 93063293.

MEDLINE; 93063293.

A CHIANO G., BENFENATI F., POULAIN B., ROSSETTO O., DE LAURETO P.P.,
A DASGUPTA B.R., MONTECUCCO C.;
I "Tetanus and botulinum-B neurotoxins block neurotransmitter release
by proteclytic cleavage of synaptobrevin.";
NATURE 359:832-835(1992).

I "TELASE: IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
RELEASE: IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
WHERE IT CAN MOVE BETWEEN POSISYNAPTIC AND PRESINAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPEPTIOSE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF
SYNAPTOBREVIN-2.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE HEAVY CHAIN MEDIATE
C-!- SUBCELLULAR LOCATION: SECRETED.
C-!- SUBCELLULAR LOCATION: SECRETED.
C-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM
NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
C-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUX NEUROTOXIN
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B, HEAVY-CHAIN.
SIMILARITY).
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                                                     MONTECUCCO
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                                                     .R.,
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BOTULINUM NEUROTOXIN B,
ZINC (CATALYTIC) (BY SI
BY SIMILARITY.
ZINC (CATALYTIC) (BY SI
INTERCHAIN (PROBABLE).
T -> M (IN REF. 4).
T -> G (IN REF. 2).
A -> S (IN REF. 2).
S -> R (IN REF. 2).
S -> R (IN REF. 4).
MW; 479BBC70 CRC32;
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                                           EDLINE; 93054694.
CHIAVO G., ROSSETTO O., SANTUCCI A., DASGUPTA
Botulinum neurotoxins are zinc proteins.";
. BIOL. CHEM. 267:23479-23483(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . No. 1.08e-
Mismatches
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INC_PROTEASE;
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             [6]
IDENTIFICATION AS ZINC-PROTEASE
MEDLINE; 93054694.
238:544
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EMBL; Z11934; G40384; -.
EMBL; Z11934; G40783; -.
PIR; S07128; S07128.
PIR; S08562; S07155.
PIR; S08562; S08562.
PIR; S08573; S08573.
PIR; S08574; S08574.
PIR; PS00142; ZINC_PROTEAPROSITE; PS00142; ZINC_PROTEAPROFO; P04958; 1AF9.
NEUROTOXIN; TRANSMEMBRANE; HY
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                                          MEDLINE;
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n near
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SEQUENCE FROM N.A.
STRAIN=NCTC 2916;
MEDLINE; 90235864.
THOMPSON D.E., BREHM J.K., OULTRAM J.D., SWINFIELD T.-J.,
SHONE C.C., ATKINSON T., MELLING J., MINTON N.P.;
SHONE C.C., ATKINSON T., MELLING J., MINTON N.P.;
"The complete amino acid sequence of the Clostridium botulinum type neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A neurotoxin gene: delineation
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MEDLINE; 85285016.
SHONE C.C., HAMBLETON P., MELLING J.;
"Inactivation of Clostridium botulinum type A neurotoxin by tranditivation of Clostridium botulinum type A neurotoxin by trand purification of two tryptic fragments. Proteolytic action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-46.
DASGUPTA B.R., FOLEY J., NIECE R.;
"Partial sequence of the light chain of botulinum neurotoxin BIOCHEMISTRY 26:4162-4162(1987).
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the heavy chain
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SEQUENCE FROM N.A.
STRAIN=62A;
MEDLINE; 90264400.
BINZ B., KUARZONO H., WILLE M., FREVENT J., WERNARS
"The complete sequence of botulinum neurotoxin type
"The complete sequence of botulinum neurotoxin type
with other clostridial neurotoxins.";
with other 265:9153-9158(1990).
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SATHYMOORTHY V., DASGUPTA B.R., FOLEY J., "Botulinum neurotoxin type A: cleavage of halves and their partial sequences."; ARCH. BIOCHEM. BIOPHYS. 266:142-151(1988).
                     1295
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                                                  P10845; P18639; P01561;
01-JUL-1989 (REL. 11, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDA
15-JUL-1998 (REL. 36, LAST ANNOTATION UP
BOTULINUM NEUROTOXIN TYPE A PRECURSOR (E
(BONTOXILYSIN A).
BOTA OR BNA.
CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDI
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. 162:1388
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STRAIN=HALL;
MEDLINE; 89350959.
BETLEY M.J., SOMERS E., DASGUPTA B.R.
"Characterization of botulinum type?"
the N-terminal encoding region.";
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SEQUENCE OF 1-16.
MEDLINE; 84178501.
SCHMIDT J.J., SARTYMOORTHY V., DA:
"Partial amino acid sequence of the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 448-464 AND 872-895.
89024662.
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MEDLINE; 91120847.
DASGUPTA B.R., DEKLEVA M.L.;
"Botulinum neurotoxin type A:
N-terminus and around the nick
BIOCHIMIE 72:661-664(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMUN
                            STANDARD;
P01561;
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SEQUENCE
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EUR. J
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                                                                RARRER REPRESENTED FOR STANDARD FOR STANDARD STA
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"Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";

J. BIOL. CHEM. 269:1617-1620(1994).

J. BIOL. CHEM. 269:1617-1620(1994).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESINAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPPRIDASE. IT CATALTZES THE HYDROLYSIS OF THE 197-GLN-|-ARG-
198 BOND IN SNAP-25.

-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL
ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE
CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM
NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM
NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
METALLOPPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM
SUPPLY METALLOPPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM
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A, HEAVY-CHAIN.
SIMILARITY).
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  toxin-binding
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E cleave SNAP-25
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BOTULINUM NEUROTOXIN A,
ZINC (CATALYTIC) (BY S)
BY SIMILARITY.
ZINC (CATALYTIC) (BY S)
INTERCHAIN (PROBABLE).
POTENTIAL.
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> K (IN REF. 6).
2E333BFB CRC32;
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1e-05;
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                                                              MEDLINE; 94063091.
SCHIAVO G., SANTTUCI A., DASGUPTA B.R.,
BENFENATI F., WILSON M.C., MONTECUCCOI (
"Botulinum neurotoxins serotypes A and )
COOH-terminal peptide bonds.";
FEBS LETT. 335:99-103(1993).
    subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90;
Pred. No.
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EMBL; M30196; G144865; -.
EMBL; M27892; G551776; -.
PIR; A35294; BTCLAB.
PIR; S09492; S09492.
PROSITE; PS00142; ZINC_PROTEASE; 1
PFAM; PF00099; Zn-protease; 1.
HSSP; P04958; 1AF9.
NEUROTOXIN; TRANSMEMBRANE; HYDROLA; INIT_MET 0 0 CHAIN 1 447 BOTUE.
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larity 57.1%;
Conservative
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                                                                                                                             FEBS LETT. 335:99-10
[10]
IDENTIFICATION OF SU
MEDLINE; 94124495.
BINZ T., BLASI J., Y
JAHN R., NIEMANN H.;
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COOH-terminus
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                          BIOCHEM.
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[AHN R., NIEMANN H.;
[Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
[Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
[F. BIOL. CHEM. 269:1617-1620(1994).
[F. BIOL. CHEM. 269:1617-1620(1994).
[F. BIOL. CHEM. BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
[FELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 92174922.
WHELAN S.M., ELMORE M.J., BODSWORTH N.J., ATKINSON T., MINTON N.P.;
"The complete amino acid sequence of the Clostridium botulinum type-E
neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-251 FROM N.A.
MEDLINE; 90264400.
BINZ T., KURAZONO H., WILLE M., FREVERT J., WERNARS K., NIEMANN H.; "The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins."; J. BIOL. CHEM. 265:9153-9158(1990).
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SEQUENCE FROM N.A.
STRAIN-BELUGA;
MEDLINE; 92181428.
POULET S., HAUSER D., QUANZ M., NIEMANN H., POPOFF M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strain ATCC 43181 and ATCC 43755).";
BIOCHEM. BIOPHYS. RES. COMMUN. 183:107-113(1992).
[2]
SEQUENCE FROM N.A.
MEDLINE; 92174922.
MEDLINE; 92174922.
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                                                                                               Q00496;
Q1-JUL-1993 (REL. 26, CREATED)
Q1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
Q1-JUL-1996 (REL. 33, LAST ANNOTATION UPDATE)
BOTULINUM NEUROTOXIN TYPE E PRECURSOR (EC 3.4.24.6
(BONTOXILYSIN E).
CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
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SCHIAVO G., SANTTUCI A., DASGUPTA B.R.,
BENFENATI F., WILSON M.C., MONTECUCCOI (
"Botulinum neurotoxins serotypes A and )
COOH-terminal peptide bonds.";
FEBS LETI. 335:99-103(1993).
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BIOCHIMIE 72:213-217(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-13.
MEDLINE; 85197963.
SCHMIDT J.J., SATHYAMOORTHY V.
"Partial amino acid sequences
E.";
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tvpe E
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MEDLINE; 94124495.
BINZ T., BLASI J., YAMASAKI
JAHN R., NIEMANN H.;
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MEDLINE; 90344918.
GIMENEZ J.A., DASGUPTA
"Botulinum neurotoxin t
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FNNFTVSFWLRVPK
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                                                      OF A LIGHT CHAIN (L) AND AS THE PHARMACOLOGICAL OF THE HEAVY CHAIN MEDIATE
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TETANUS/BOTULINUM NEUROTOXIN
                AS A ZINC
OF THE 180-ARG-|-ILE
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E, HEAVY-CHAIN
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                                                                                                                   FORMS OF BOTULINUM
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       PRESYNAPTIC
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                                   181 BOND IN SNAP-25.

!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAN A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOL ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

!- SUBCELLULAR LOCATION: SECRETED.

!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTU NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINU
                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROLASE; METALLOPROTEASE;
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BOTULINUM NEUROTOXIN E,
ZINC (CATALYTIC) (BY SI
BY SIMILARITY.
ZINC (CATALYTIC) (BY SI
INTERCHAIN (PROBABLE).
R -> G (IN REF. 2).
C -> S (IN REF. 2).
T -> L (IN REF. 2).
I -> L (IN REF. 2).
FE -> LQ (IN REF. 2).
FE -> LQ (IN REF. 2).
N -> NN (IN REF. 2).
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INHIBITS NEUROTRANSMITTER RELEASE BY ACTING ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS 181 BOND IN SNAP-25.
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Pred. No. 1.11e-04
7; Mismatches (
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
TYPE E PRECURSOR (EC 3.4
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EMBL; X62683; G40398; -.

PIR; A60027; A60027.

PIR; B35294; B35294.

PIR; B35294; B35294.

PIR; S08575; JH0257.

PIR; S18111; S18111.

PIR; S21178; S21178.

PROSITE; PS00142; ZINC_PROTEASE; 1

PFAM; PF00099; Zn-protease; 1.

HSSP; P04958; 1AF9.

NEUROTOXIN; TRANSMEMBRANE; HYDROLA
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Conservative
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01-JUL-1993 (REL. 26, CR 01-JUL-1993 (REL. 26, LA 01-NOV-1995 (REL. 32, LA BOTULINUM NEUROTOXIN TYH (BONTOXILYSIN E).
CLOSTRIDIUM BUTYRICUM.
ÉACTERIA: FIRMICUTES; BACLOSTRIDIUM.
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SEQUENCE FROM N.A

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STRAIN=5262;

GIMENEZ J., FOLEY J., DASGUPTA B.R.;

"Neurotoxin type E from Clostridium botulinum and C. butyricum;

partial sequence and comparison.";

FASEB J. 2:A1750-A1750(1988).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPEPTIDASE.

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neurotoxin E derived from Clostridium
.uga) and Clostridium butyricum (strains
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HEAVY-CHAIN
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E, HEAVY-CHA
SIMILARITY).
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BL6340.
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SUBCELLULAR LOCATION: SECRETED.

THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULI NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM
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                                                                                                                                                                                 BIOCHEM.

[2]
SEQUENCE OF 1-251 FROM .

STRAIN=BL6340;
MEDLINE; 91237316.

A FUJII N., KIMURA K., MURAKAMI T., INDOH T., ...

A YOKOSAWA N., YASHIKI T., OGUMA K.;
"Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of a DNA fragment encoding the 5'-terminus of "Cloning of "
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EMBL; X53180; G40408; ".
PIR; JH0256; JH0256.
PIR; S16145; S16145.
PROSITE; PS00142; ZINC_PROTEASE; 1
PFAM; PF00099; Zn-protease; 1.
HSSP; P04958; 1AF9.
NEUROTOXIN; TRANSMEMBRANE; HYDROLA
STRAIN=ATCC 43181, AND ATCC 43755;
MEDLINE; 92181428.
POULET S., HAUSER D., QUANZ M., NI.
"Sequences of the botulinal neurotic botulinum type E (strain Beluga) a ATCC 43181 and ATCC 43755).";
BIOCHEM. BIOPHYS. RES. COMMUN. 183
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IS THE
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VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; BUNYAVIRIDAE; TOSPOVIRUS
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                                                                                            HORSE SICKNESS VIRUS 6 (AHSV-6) (AFRICAN HORSE SICKNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                    WILLIAMS C.F., INOUE T., LUCUS A.-M., ZANOTTO P., ROY P.,
"The complete sequence of four major structural proteins of
horse sickness virus serotype 6: evolutionary relationships
and between the orbiviruses.";
VIRUS RES. 53:53-73(1998).

-!- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WI
WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS
MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.

-!- SIMILARITY: BELONGS TO THE THE REOVIRUSES VP2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1051;
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FUNCTION: FORMS FILAMENTOUS INCLUSION BODIES.
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               VP2_AHSV6 STANDARD; PRT; 1051 AA.
071024;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
00TER CAPSID PROTEIN VP2.
S2 OR L2.
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DSRNA VIRUSES; REOVIRIDAE; ORBIVIRUS
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01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
NONSTRUCTURAL PROTEIN NS-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87;
Pred. No.
                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE: 98278331.
WILLIAMS C.F., INOUE T., LUCUS A.-M.,
"The complete sequence of four major;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAGEMAKERS L., PETERS D.,
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larity 47.6%;
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les 10; Conse
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VNSS_TSWV1
P26002;
01-MAY-1992
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01-JUN-1994
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AFRICAN HOI
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VIRUSES; D:
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VIRUSES; BUNYAVIRIDAE; TOSPOVIRUS
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                                                                                Length
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SEQUENCE FROM N.A.
MEDLINE; 91132150.
MAISS E., IVANOVA L., BREYEL E., ADAM G.;
"Cloning and sequencing of the S RNA from a Bulgaria tomato spotted wilt virus.";
J. GEN. VIROL. 72:461-464(1991).
-!- FUNCTION: FORMS FILAMENTOUS INCLUSION BODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROUP;
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H
                                                                             e 84; DB 1; L
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Mismatches 1
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-04
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                      SPOTTED WILT VIRUS (STRAIN); SSRNA NEGATIVE-STRAND VI
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larity 64.3%;
Conservative
                                                                                                                                                                                                                                                                                                         NS-S
                                               2448
                                                                           Similarity 64.38, 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 90370487.
HAUSER D., EKLUND M.W., F
BOQUET P., POPOFF M.R.;
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256
EMBL; D00645; D1000995
PIR; JQ0547; MNVUWC.
NONSTRUCTURAL PROTEIN.
SEQUENCE 464 AA; 52.
                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D13926; G222683; PIR; JQ0954; MNVUW1. NONSTRUCTURAL PROTEIN. SEQUENCE 467 AA; 52.
                                                                                                                                                                                                                                                            255
29,
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CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES;
CLOSTRIDIUM.
                                                                                                                                                                                                                                                                                                      NONSTRUCTURAL PROTEIN
                                                                                                                                        SHFKLSLWLRVPKY
                                                                                                                                                     SHFKLSLWLRVPKV
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neurotoxin.";

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Clostridium botulinum

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                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94038966.

MEDLINE; 94038966.

MEDLINE; 94038966.

BLASI J., CHAPMAN E.R., YAWASAKI S., BINZ T., NIEMANN H., JAHN R.;

"Botulinum neurotoxin.";

Cleaving HPC-1/syntaxin.";

EMBO J. 12:4821-4828(1993).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERFUBERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.

C. SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L.) AND A

A HEAVY CHAIN (H.). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL

A CTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE

C. SUBCELLULAR LOCATION: SECRETED.

C. SUBCELLULAR LOCATION: SECRETED.

C. SUBCELLULAR LOCATION: SECRETED.

C. SUBCELLULAR LOCATION: SECRETED.

C. SUBCELLULAR BOTULINUM WHICH CARRY THE APPROPRIATE BACTERIOPHAGE.

C. SUBCIRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE BACTERIOPHAGE.

C. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC

METALLOPPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
                                                                                                         for botulinum
                                                                                                                                                                                                                                               W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIGHT-CHAIN
HEAVY-CHAIN
                                                                                                                                                                                                                                            n antigenic
toxins and
                                                                                                                                                                                                                 SYUTO B., OHISHI I., FUJII N., KIMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C1, LIGHT-CH
C1, HEAVY-CH
SIMILARITY).
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EMBL; X72793; G516175; -.

EMBL; X53751; G14906; -.

EMBL; X62389; G40390; -.

EMBL; X62389; G40390; -.

PIR; X1291; S11291.

PIR; A43503; A43503.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PFAM; PF00099; Zn-protease; 1.

NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; ZIN INIT_MET 0 0
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BOTULINUM NEUROTOXIN C1,
ZINC (CATALYTIC) (BY SIN
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIN
INTERCHAIN (PROBABLE).
P -> T (IN REF. 2).
                                                                                                                                                                                                                                                             闪
                                                                                                         coding
                                                                                                                                                                                                                                             recognizing C1, D, and
                                                                                                                        genome.";
171:1304-1311(1990)
                                                         MEDLINE; 91024998.
KIMURA K., FUJII N., TSUZUKI K., MURAKAMI T.,
YOKOSAWA N., TAKESHI K., SYUTO B., OGUMA K.;
"The complete nucleotide sequence of the gene
type C1 toxin in the C-ST phage genome.";
RIOCHEM. BIOPHYS. RES. COMMUN. 171:1304-1311(
                                                                                                                                                                                                MEDLINE; 88153072.

TSUZUKI K., YOKOSAWA N., SYUTO B., OHISHOGUMA K.;
"Establishment of a monoclonal antibody common to Clostridium botulinum type B, tetanus toxin.";
INFECT. IMMUN. 56:898-902(1988).
18:4924-4924(1990)
                                                                                                                                                                    2-25.
C STOCKHOLM / C-ST;
153072.
                                             ů
                                                                                                                                                                                                                                                                                                                         OF SUBSTRATE
                              FROM N.A.
YPE C STOCKHOLM 91024998.
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222
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222
48
232
88
8223
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IDENTIFICATION OF:
MEDLINE; 94038966.
ACIDS RES
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22224
2323
48
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                                                                                                                                                                   SEQUENCE OF 2-
STRAIN=TYPE C
MEDLINE; 88153
                                             STRAIN=TYPE MEDLINE; 91
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BIOCHEM.
[3]
                                 UENCE
NUCLEIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOSPOVIRUS
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THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=TYPE C STOCKHOLM / C-ST;
MEDLINE; 92231894.
TSUZUKI K., KIMURA K., FUJII N., YOKOSAWA N., OGUMA K.;
TSUZUKI K., KIMURA K., FUJII N., YOKOSAWA N., OGUMA K.;
TSUZUKI K., KIMURA K., FUJII N., YOKOSAWA N., OGUMA K.;
TSUZUKI K., KIMURA K., FUJII N., YOKOSAWA N., OGUMA K.;
"The complete nucleotide sequence of the gene coding for the nontoxic-nonhemagglutinin component of Clostridium botulinum progenitor toxin.";
BIOCHEM. BIOPHYS. RES. COMMUN. 183:1273-1279(1992).
-!- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \circ
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                                             1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 449;
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                                                                                              Indel
                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STRAIN NL-07) (INSV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Impatiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e 77; DB 1; Len ... No. 1.51e-02; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BODIES
  D0BCB190 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BXCN_CLOBO STANDARD; PRT; 1196 AA.
P46081;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
BOTULINUM NEUROTOXIN TYPE C1, NONTOXIC COMPONENCE COSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUI
                                                                       -03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6A87666F CRC32;
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UPDATE
                                               e 81; DB 1;
. No. 2.63e-
Mismatches
                                                                                                                                                                                                                                                                                               449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus, a nover corrections.

FEBS LETT. 306:27-32(1992).

-!- FUNCTION: FORMS FILAMENTOUS INCLUSION

-:- FUNCTION: TORMS FILAMENTOUS INCLUSION
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Pred. No.
5; Misma
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ANNOTATION
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Pred.
7; M
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MEDLINE; 92331780.
DE HAAN P., DE AVILA A.C., KORMEL
GIELEN J.J., PETERS D., GOLDBACH
"The nucleotide sequence of the S
virus, a novel tospovirus.";
FEBS LETT. 306:27-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.C., AV.,
GOLDBACH
                                                                                                                                                                                                                                                                                                                              U1-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUE.
01-JUN-1994 (REL. 29, LAST ANNOT.
NONSTRUCTURAL PROTEIN NS-S.
NS.
IMPATIENS NECROTIC SPOT VIRUS (STATUSES; SSRNA NEGATIVE-STRAND V.
[1]
MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X66972; G60489; -.
PIR; S23158; S23158.
NONSTRUCTURAL PROTEIN.
SEQUENCE 449 AA; 51197 MW;
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Larity 50.0%;
Conservative
  148734
                                               51.3%;
Larity 42.9%;
Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                  YESFSISFWIRINK
   AA;
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FTVSFWLRVPKV
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  1290
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VNSS_INSVN
Q01811;
01-JUL-1993
01-JUL-1993
01-JUN-1994
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Matches
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Matches
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MEDLINE; 94230352.

YAMASAKI S., BAUMEISIER A., BINZ T., BLASI J., LINK E., CORNILLE F., ROQUES B., FYKSE E.M., SUEDHOF T.C., JAHN R., NIEMANN H.; ROQUES B., FYKSE E.M., SUEDHOF T.C., JAHN R., NIEMANN H.; "Cleavage of members of the synaptobrevin/VAMP family by types D and F botulinal neurotoxins and tetanus toxin."; F botulinal neurotoxins and tetanus toxin."; J. BIOL. CHEM. 269:12764-12772(1994).

J. BIOL. CHEM. 269:12764-12772(1994).

FLUCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
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OHYAMA I., WAIANABE I., INOUE K.;
samino acid sequence of the Clostridium botulinum type
leduced by nucleotide sequence analysis of the encoding
ni genome.";
SCI. 54:905-913(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGUMA K.;
ins from Clostridium botulinum type
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROUP; CLOSIRIDIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POPOFF M.R., EKLUND M.W., SAKAGUCHI G.,
N K., HENSCHEN A., GILL D.M., NIEMANN H.;
of the gene encoding Clostridium botulinum
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                                                                                                                                                                                                                           0;
                                                                                                                                                                                                  Length 1196;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                        .24.69)
                                                                                                                                                                    E5C11933 CRC32;
                                                                                                                                                                                                e 76; DB 1; Le
. No. 2.32e-02;
Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           P19321;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
BOTULINUM NEUROTOXIN TYPE D PRECURSOR (EC 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACILLUS/CLOSTRIDIUM
                                                                                                                                                                                                                                                                                                                                      1276
                                                                                                                                                                                             Score 76;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18:5556-5556(1990)
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                                                                                                                                                                  MW;
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                                                                                                                                                                   138740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., KUBO .
                                                                                                                                                                                             48.1%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BVD/-3;
MEDLINE; 91016853.
BINZ T., KURAZONO H., POPC
KOZAKI S., KRIEGLSTEIN K.,
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-1873;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BOTULINUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYUTO B.,
                                                                                                                                    EMBL; X62389; G40389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIRMICUTES;
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MEDLINE; 89339741.
MORIISHI K., SYUTO B.,
"Molecular diversity o
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deduced
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RES. 1
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"The complete amino
neurotoxin, deduced
phage d-16 phi genor
J. VET. MED
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  TOXICITY.
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KOZAKI S., KH
"Nucleotide s
neurotoxin ty
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SEQUENCE
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BACTERIA; FI
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MEDLINE; 93
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CLOBO
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INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE THAT CLEAVES THE 60-LYS-|-LEU-61 BOND OF SYNAPTOBREVINS-1 AND -2.

SYNAPTOBREVINS-1 AND -2.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.

-!- BOTULINUM TYPE D NEUROTOXIN IS SYNTHESIZED BY D STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE BACTERIOPHAGE.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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BOTULINUM NEUROTOXIN D, HEAVY-CHAIN.
ZINC (CATALYIIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYIE).
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ZINC (CATALYTIC) (BY SIMILARI
INTERCHAIN (PROBABLE).

ND -> PV (IN STRAIN D-SA).

K -> Q (IN STRAIN D-1873).

K -> Q (IN STRAIN D-SA).

R -> T (IN STRAIN D-SA).

R -> F (IN STRAIN D-1873).

R -> D (IN STRAIN D-1873).

K -> N (IN STRAIN CB16).

N -> K (IN STRAIN CB16).

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Q -> R (IN STRAIN CB16).
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Mismatches
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Pred. No.
9; Misma
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EMBL; S49407; G260239; -.
PIR; S11455; S11455.

PROSITE; PS00142; ZINC_PROTEASE; 1
PFAM; PF00099; Zn-protease; 1.
NEUROTOXIN; TRANSMEMBRANE; HYDROLA
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BACTERIA; FIRMICUTES;
CLOSTRIDIUM.
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MEDLINE; 93195515.
FUJII N., KIMURA K
"The complete nucle
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OGUMA K.; nontoxic

K., the

TSUZUKI K encoding

r., gene

YASHIKI Of the q the

N., KIMURA K., YOKOSAWA N., complete nucleotide sequence

OGUMA

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EMBL; D12697; G285708; -.

EMBL; D12697; G285708; -.

SEQUENCE 1162 AA; 136856 MW; F650831D CRC32;
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                                     toxin.";
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component of Clostridium botulinum type E progenitor
J. GEN. MICROBIOL. 139:79-86(1993).
-!- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO
TOXICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 1; Le
Pred. No. 2.84e-01;
2; Mismatches 1;
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larity 70.0%;
Conservative
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Search completed: Tue Aug 17 15:54:43 1999 Job time: 15 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.25 Seconds 183.290 Million cell updates/sec Tue Aug 17 15:55:01 1999; ou:

not generated. output Tabular

>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

residues 54579741 seds, 179066 Searched:

Post-processing:

summaries Minimum Match 0% Listing first 45

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Variance 45.917; Mean 29.394;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. scale 0.540 Statistics:

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ALIGNMENTS

PRELIMINARY; PRT; 1; 1996 (TREMBLREL. 01, CREATED) 1998 (TREMBLREL. 08, LAST ANNO) XIN TYPE F. DIUM BARATI. A; FIRMICUTES; BACILLUS/CLOSTR3 DIUM. E FROM N.A. 9325228. N D.E., HUTSON R.A., EAST A.K., SON P.T.; tide sequence of the gene codin tide sequence of the gene codin xin: comparison with other clos CROBIOL. LETT. 108:175-182(1993; CROBIOL. LETT. 108:175-182(1993; E 1268 AA; 145512 MW; 37B7A h, 60.1%; Score 95;	Local Similarity 64.3%; Pred. No. 1.58e-05; es 9; Conservative 4; Mismatches 1; Ind 22 YQNFSVSFWVRIPK 935 : : :
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SIMILARITY:
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SEQUENCE FROM N.A.
STRAIN=NCTC 10281;
HUTSON R.A., COLLINS M.D.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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                                                                    the botulinal kin types B, E
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                                                                                                                                                                                                                                                                                                                                                                                                                   CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIU
CLOSTRIDIUM.
[1]
SEQUENCE FROM N.A.
STRAIN=TYPE B, NON-PROTEOLYTIC 2129B (SCC MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.; "Gene probes for identification of the bc specific identification of neurotoxin type J. CLIN. MICROBIOL. 31:2255-2262(1993).
EMBL; X70814; G407779; -.
NEUROTOXIN.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=TYPE B, NON-PROTECLYTIC EKLUND 2B
MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.;
"Gene probes for identification of the bospecific identification of neurotoxin typurocinic identification of neurotoxin identification of neurotoxin typurocinic identification of neurotoxi
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4; M
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Pred.
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CLOSTRIDIUM BOTULINUM.

CLOSTRIDIUM.

CLOSTRIDIUM.
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EL. 08,
TYPE E
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64.3%;
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01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPEPTIDASE THAT CLEAVES SYNAPTOBREVIN-2.

-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN

(L) AND A HEAVY CHAIN (H).

THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-
AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXINS AND WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILE
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for non-proteolytic
comparison with other
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                                                                                                                                                                                                                                                                                    neurotoxin and F.";
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EMBL; X71343; G296149; -.

PFAM; PF00099; Zn-protease; 1.

PFAM; PF00099; Zn-protease; 1.

NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE;

NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE;
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                               MINTON N.P
DATA BANKS
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
(EC 3.4.24.-) (BONT/B)
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No. 3.93e-05;
Mismatches 1
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SEQUENCE FROM N.A.

STRAIN=EKLUND 17B ATCC25765;

MEDLINE; 94122659.

HUTSON R.A., COLLINS M.D., EAST A.K., THOMP:
"Nucleotide sequence of the gene coding for Clostridium botulinum type B neurotoxin: coclostridial neurotoxins.";

CURR. MICROBIOL. 28:101-110(1994).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIE RELEASE.

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THELEASE.

THOMP:

THOMP:

STRAIN ACTS BY INHIE ACTS BY I
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                                                                                                                             SEQUENCE OF 635-1000 FROM N.A.
STRAIN=TYPE F, PROTECLYTIC F LANGELAND (NC MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.;
"Gene probes for identification of the bot specific identification of neurotoxin typespecific identification of neurotoxin typespecific identification of neurotoxin typespecific identification of neurotoxin typespecific identification of neurotoxin typesmbL; X81714; G971349; -.
EMBL; X81714; G971349; -.
EMBL; X70821; G407793; -.
PFAM; PF00099; zn-protease; 1.
                                 I.J., WHELAN S.M.,
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93;
Pred. No.
5; Misma
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Local Similarity 57.1%;
les 8; Conservative
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(TREMBLREL.
(TREMBLREL.
FROM N.A.
J., BODSWORTH N
(AUG-1994) TO I
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O08077;
O1-NOV-1996 (TREMBLREL
01-NOV-1996 (TREMBLREL
01-NOV-1998 (TREMBLREL
BOTULINUM NEUROTOXIN T
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CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES;
CLOSTRIDIUM.
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FNNFTVSFWLRVPK
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1291

Best Loc Matches

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SEQUENCE OF 1-65 FROM N.A.

STRAIN=62A;

MEDLINE; 97016817.

A EAST A.K., BHANDARI M., STACEY J.M., CAMPBELL K.D., COLLINS M.D.;

Components of the botulinum toxin complex in proteolytic clostridium tomponents of the botulinum toxin complex in proteolytic clostridium town types A, B, and F: evidence of chimeric sequences in the potulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

INT. J. SYST. BACTERIOL. 46:1105-1112(1996).

EMBL; X73423; G507071; -.

EMBL; X87974; E184381; -.

NEUROTOXIN.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=KYOTO-F;
MEDLINE; 94143603.
WILLEMS A., EAST A.K., LAWSON P.A., COLLINS M.D.;
"Sequence of the gene coding for the neurotoxin of botulinum type A associated with infant botulism: cother clostridial neurotoxins.";
RES. MICROBIOL. 144:547-556(1993).
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reassortment
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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2.13e-03;
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Mismatches
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Mismatches
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MEDLINE; 98240946.
QIU W.-P., GESKE S.M., HICKEY C.M., MOYEF
"Tomato spotted wilt Tospovirus genome re
segment-specific adaptation.";
VIROLOGY 244:186-194(1998).
EMBL; AF020660; G2425149; -.
SEQUENCE 467 AA; 52587 MW; 1D153724 C
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NEGATIVE-STRAND VIRUSES;
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Pred. No.
6; Misma
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Pred. No.
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                                                                           Q45894 PRELIMINARY;
Q45894; P77780;
O1-NOV-1996 (TREMBLREL. 01, L2
O1-NOV-1998 (TREMBLREL. 08, L2
BOTULINUM NEUROTOXIN TYPE A.
BONT.
CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS
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037369;
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
NON-STRUCTURAL PROTEIN.
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                  FNNFTVSFWLRVPK
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VIRUSES; SSRNA NEG:
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SEQUENCE FROM N.A.
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AC Q45862

AC Q45862

DT O1-NOV-1996 (TREMBLREL. 01, CREATED)

DT O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE BOTULINUM NEUROTOXIN TYPE E (FRAGMENT).

GN BONT/E.

CLOSTRIDIUM BOTULINUM.

OC CLOSTRIDIUM.

OC CLOSTRIDIUM.

RA CLOSTRIDIUM.

RY SEQUENCE FROM N.A.

RX MEDLINE; 94013372.

RX MEDLINE; 94013372.

RA CAMPBELL K., EAST A.K., COLLINS M.D.;

RY "Gene probes for identification of the botulinal neurotoxin gene and RD. CLIN. MICROBIOL. 31:2255-2262(1993).

RY NOW_TER 1

FT NON_TER 247787; ...

RA CAMPBELL STORES AND STORE
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Q45851
Q45861;
Q45861;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
Q1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
BOTULINUM NEUROTOXIN TYPE E (FRAGMENT).
CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIUM.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(FRAGMENT).
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SEQUENCE FROM N.A.
STRAIN=TYPE E, VH (DOLMAN);
MEDLINE; 94013372.
CAMPBELL K., EAST A.K., COLLINS M.D.;
"Gene probes for identification of the botulinal rypers for identification of neurotoxin types B, E, J. CLIN. MICROBIOL. 31:2255-2262(1993).
EMBL; X70818; G407785; -.
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. No. 3.68e-04;
Mismatches 0
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SEQUENCE FROM N.A.
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C Q45967;
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T 01-NOV-1996 (TREMBLREL. 01, CREATED)
T 01-NOV-1999 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
T 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
S CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTPITATION.
[11]
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                                                                                                               VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; BUNYAVIRIDAE; 1 [1]
SEQUENCE FROM N.A.
STRAIN=TSWV-10;
MEDLINE; 98240946.
QIU W.-P., GESKE S.M., HICKEY C.M., MOYER J.W.;
"Tomato spotted wilt Tospovirus genome reassortment and segment-specific adaptation.";
VIROLOGY 244:186-194(1998).
EMBL; AF020659; G2425152; -.
SEQUENCE 467 AA; 52505 MW; B3A4243F CRC32;
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Mismatches 1
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. No. 2.13e-03
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NEGATIVE-STRAND VIRUSES;
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larity 64.3%;
Conservative
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01-NOV-1998 (TREMBLREL. 0
NON-STRUCTURAL PROTEIN.
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STRAIN=ISWV-B;
PANG S.Z., SLIG
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UNKNOWN.
VIRUSES; SSRNA
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Q88900;

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01-NOV-1996

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037367;
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01-JAN-1998
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EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITI
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                     \searrow
                     INOUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BANKS
                                                                                                                                        Length
                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                     ABE N., FUJII N., FUJINAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 79; DB 5; Lei
Pred. No. 1.80e-02;
3; Mismatches 0;
                                                                                                                  CRC32;
                                                                                                                                                      ** ==
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                       e 81; DB 2; L
. No. 7.72e-03;
Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B4E0F90C CRC32;
                                                                                                                                                                                                                                                              AA
                                        neurotoxins produced
                                 OGUMAD K.;
"Mosaic structures of neurotoxins produce
types C and D organisms.";
BIOCHIM. BIOPHYS. ACTA 1307:123-126(1996)
EMBL; D38442; D1008057; -.
PFAM; PF00099; zn-protease; 1.
                                                                                                                   381133E1
                                                                                                                                                                                                                                                            322
                                                                                                                                       Score 81;
Pred. No.
7; Misma
                                                                                                                                                                                                                                                            PRT;
                                                                                                                   MW;
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AFRICAN;
                                                                                                                                                                                                                                                                                   03,
03,
08,
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(DEC-1996) TO E...
042; G1707209; -...
                                                                                                                    147366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 70.0%; 7; Conservative
                                                                                                                                        51.3%;
larity 42.9%;
Conservative
                                                                                                                                                                                                                                                  P91551 PRELIMINARY;
P91551;
01-MAY-1997 (TREMBLREL. (
01-MAY-1997 (TREMBLREL. (
01-NOV-1998 (TREMBLREL. (
COSMID ZC239.
                                                                                                                                                                                                                                                              PRELIMINARY;
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SUBMITTED (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
WATERSTON R.;
SUBMITTED (DEC-1996
EMBL; U80842; G1707
SEQUENCE 322 AA;
                                                                                                                                                                                         931 YESFSISFWIRINK
                                                                                                                                                                                                              1 FNNFTVSFWLRVPK
                                                                                                                   1285 AA;
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                       KOURA
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D 05350
C 05350
T 01-NOV-1996 (TREMBLREL. 01, CREATED)
T 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
T 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
T CLOSTRIDIUM BOTULINUM.

C CLOSTRIDIUM BOTULINUM.

C CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
T (1)
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Q45916
Q45916;
Q45916;
O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. O7, LAST ANNOTATION UPDATE)
138KDA PROTEIN ASSOCIATED WITH BONT /C1-HAEMAGGLUTININ
CHN-138.
CLOSTRIDIUM BOTULINUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOST
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
HAUSER D.F., EKLUND M.W., POPOFF M.R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; X66433; G509274; -.
SEQUENCE 1194 AA; 138509 MW; 0192832A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76; DB 2; Ler
Pred. No. 6.29e-02;
1; Mismatches 1;
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Pred. No. 6.29e-02;
1; Mismatches 1;
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Best Local Similarity 80.0%;
Matches 8; Conservative
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2 NNFTVSFWLR 11
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Search completed: Tue Aug 17 15:55:46 1999 Job time : 45 secs.

11

NNFTVSFWLR

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(MI)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Smith-Waterman algorithm search, using database protein protein MPsrch_pp

MasPar time 6.95 Seconds 152.315 Million cell updates/sec Tue Aug 17 16:18:07 1999;

not generated. output Tabular

Run on:

>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21

Description: Perfect Score: Sequence:

PAM 150 Gap 15 table: Scoring

residues 50406085 seds, 411786 Searched:

summaries Minimum Match 08 Listing first 45 Post-processing:

Database:

a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B
10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92
18:U93 19:NEWP 20:NEWU6 21:NEWU8 22:NEWU9

0.300 scale Variance 74.265; Mean 22.277; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	.00e-0	.00e-0	.00e-0	.00e-0	.00e-0	1.00e-08	.00e-0	.00e-0	.00e-0	1	.00e-0	.00e-0	.00e-0	.00e-0	0.00e-0	.00e-0	.00e-0	.00e-0	.00e-0	1.00e-08	.00e-0
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	Description	Sequence 3,	Sequence 3,	Sequence 1,	Sequence 2,	Sequence 10	e G	ence 4	ce	ednence 3	Sequence 66		ednence	ce 2	ednence	equence 3	ce 4	Sequence 40	equence 4	ence 6	Sequence 64	Sequence 14
SUMMARIES	QI	US-08-432-	4	9-10-	-04	-09-1	S-08-	S - 08 - 40		-08-43	S-08-1	-08-24	0-	-08-57	0-	90-60-	90-	-06	0-60-	US-08-161-	-16	US-08-229-
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  FEATURE.

NAME/KEY: 21 ...

NAME/KEY: helper T c...

LOCATION:

PUBLICATION INFORMATION:

AUTHORS: Panina-Bordignon, P., et al.

TITLE: Universally immunogenic T cell

TITLE: epitopes: promiscuous binding to human MHC cli

TITLE: promiscuous recognition by T cells

JOURNAL: European Journal of Immunology

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A:FROM 1 TO 21
                                                                                                                                                                                                                                                               APPLICANT: Rittershaus, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
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                                                                                                                                         Indels
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1.00e-08;
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                                                                                                                                         Mismatches
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APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
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Cambridge
                                                                                                                          Score 158;
Pred. No. 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Leon R. Yankwich REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
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CHARACTERISTICS:
1: 21 amino acids
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                                                                                                                                                                                               STANDARD;
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APPLICATION NUMBER:
FILING DATE: May 1,1
ATTORNEY/AGENT INFORMAT
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INFORMATION:
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OPERATING
SOFTWARE:
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CITY: Ca
STATE: M
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GENERAL INFORMATION:
APPLICANT: Antonello PESSI
APPLICANT: Elisabetta BIANCHI
APPLICANT: Giampietro CORRADIN
TITLE OF INVENTION: IMMUNOGENIC COMPOUNDS, THE PR
TITLE OF INVENTION: THEIR SYNTHESIS AND THEIR USE
TITLE OF INVENTION: ANTIMALARIA VACCINES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                       tetanus
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Universally immunogenic
European Journal of Ir
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1990
                                                                                                                                             CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/67
FILING DATE: 01 Apr 1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT 19914
FILING DATE: 02 Apr 1990
CLASSIFICATION: 424
TELECOMMUNICATION: 424
TELEPHONE: (212) 827-3000
TELEFAX: (212) 840-6702
                                                                                                                                                                 Score
Pred.
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ZIP: 10020-1193
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
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New York
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7-678-684B-1
                    NAME/KEY:
LOCATION:
PUBLICATION:
AUTHORS:
ANTI-SENSE:
FEATURE:
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CITY: Ne
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                                                                                                                               Sequence 2, Application US/09049847
GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Cantacuzene, Daniele
APPLICANT: Lo-Man, Richard
IITLE OF INVENTION: Mutiple antigen alycopeptide car
IITLE OF INVENTION: Comprising the same and use ther
FILE REFERENCE: 102.166A
CURRENT APPLICATION NUMBER: US/09/049,847
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/041,726
EARLIER FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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 Score 158; DB 3;
Pred. No. 1.00e-08;
0; Mismatches ()
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Pred. No. 1.00e-08
0; Mismatches
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PLASMID-BASED
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09171969 GENERAL INFORMATION:
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                                                                                                                   Application US/09049847
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TITLE OF INVENTION: PL,
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                            h
Similarity 100.0%;
21; Conservative
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AA; 2479 MW;
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Best Local Similarity 100.0%;
Matches 21; Conservative
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US-09-171-969-10
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CITY: BO
STATE: M
COUNTRY:
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US-09-049-847
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i. Donata; Jongeneel, Victor; C
i. Cerrottini, Jean-Charles; Car
i. Reed, Daryl
i. MAGE-10 ENCODING CDNA, The T
i. Rejection Antigen Precuros M
i. Antibodies Specific To The M
i. Uses Thereof

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Pred. No. 1.00e-08
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              MBER: US/09/171,969
01 May 1997 (01.05.97)
                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
                                                                                                                                                                                                 414.1
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03-October-1996
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oruary 1997
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SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                     FILING DATE: 21 February
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 03-October-19
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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805 Third Avenue
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Similarity 100.0%;
21; Conservative
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                        APPLICATION NUMBER:
FILING DATE: 01 May
CLASSIFICATION: 51
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Pierre; C
Stefan; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rimoldi,
APPLICANT: Pierre; CAPPLICANT: Stefan; FITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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COMPUTER: IBM
OPERATING SYSTEM:
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HYPOTHETICAL:
ANTI-SENSE:
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US-09-049-847

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FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,889A
FILLING DATE: 02-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
                                                                                                                                                                                       Sequence 66, Application US/08161889A
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                  Epitopes
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T: 4560 Horton S
Emeryville
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INFORMATION FOR
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STREET: 45
CITY: Emer
STATE: CA
COUNTRY: U
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No. 1.00e-08;
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DX
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
COMPUTER: IBM PS/2 COMPATIBLE 486 DX
OPERATING SYSTEM: MS DOS 6.2
SOFTWARE: WORDPERFECT FOR MS DOS 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,916B
FILING DATE: 27 MAR 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08370
FILING DATE: 30 SEP 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 22,773
REFERENCE/DOCKET NUMBER: URF 2 056 3
TELEPHONE: (614) 575 2100
TELEPHONE: (614) 575 2149
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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. No. 1.00e-
Mismatches
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                     5457
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NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                 US/08406916B
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                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08406916
GENERAL INFORMATION:
APPLICANT: STEVENS, VERNON C.
TITLE OF INVENTION: VACCINES AI
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLARD, SIDNEY W
STREET: 7632 SLATE RIDGE BOUI
CITY: REYNOLDSBURG
STATE: OHIO
COUNTRY: USA
ZIP: 43068
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                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21
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SEQUENCE 21 AA; 2479 MW;
                                                                                                                                100.0%;
larity 100.0%;
conservative
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2479 MW;
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TOPOLOGY: li
MOLECULE TYPE:
DESCRIPTION:
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 Length
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Score 158; DB 8; L. Pred. No. 1.00e-08; 0; Mismatches 0;
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Pred. No. 1.00e-08
0; Mismatches
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                                                                                                                             STATE: C. COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,889
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-655-3542
TELEPHONE: 510-655-3542
TELEPHONE: TOR SEQ ID NO: 66:
                                                                    Epitopes
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Composition a
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                    luence 66, Application US/0816188
NERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08245507
 US/0816188
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                                                                                        STATE: CA
                                            , H. Mario
Stuart J.
: T-Cell E
S: 75
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Hodges, Robert
^~^hia, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                APPLICANT: Geysen, H. ..
APPLICANT: Rodda, Stua:
TITLE OF INVENTION: T-(
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant
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2479 MW· ^
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Best Local Similarity 100.0%;
Matches 21; Conservative
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Application
                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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TOPOLOGY: lin
MOLECULE TYPE:
SEQUENCE 21 AA; 24
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US-08-245-507-14
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                                                 yuence 3, Application US/08432483
sNERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 21-amino acid tetanus toxoid
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Panina-Bordignon, P., et
TITLE: Universally immunogenic T cell
TITLE: epitopes: promiscuous binding to human MHC
TITLE: promiscuous recognition by T cells
TITLE: promiscuous recognition by T cells
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1.00e-08;
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Journal of Immunology
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South Wacker Drive
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Pred. No. 1
0; Mismat
                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN;
                              US/08432483
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2810
                                                                                                                                                                                                                                                                                                                                           NAME: Leon R. Yankwich REGISTRATION NUMBER: 30,2 REFERENCE/DOCKET NUMBER: FORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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larity 100.0%;
Conservative
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PRIOR APPLICATION DATA
FILING DATE:
ATTORNEY/AGENT INFORMAT
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FILING DATE:
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19
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3Y: linear
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                              Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 2237-2242
DATE: 1989
RELEVANT RESIDUES
SEQUENCE 21 AA; 2479 N
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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US-08-161-889-66
                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL:
VOLUME:
ISSUE:
PAGES: 2
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GENERAL
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Best Local S
Matches 2
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SOFTWARE:
CURRENT APPL
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Molecule,
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Mismatches
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R: 33,875
TTTR: 8900-0009
                 Suite
 Associates
                                                                                                                                                                                       US/08/245,507
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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Pred. No. 1
0; Mismat
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GENERAL INFORMATION:
APPLICANT: Rimoldi, Donata; Jonger
APPLICANT: Pierre; Cerrottini, Jez
APPLICANT: Stefan; Reed, Daryl
TITLE OF INVENTION: MAGE-10 ENCOD:
TITLE OF INVENTION: Rejection Ant:
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen,
                                                                                                                                                                                APPLICATION NUMBER: US/08/245
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
                 Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN;
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MEDIUM TYPE: Diskette,
COMPUTER: IBM
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ADDRESSEE: Dehlinger & STREET: 350 Cambridge CITY: Palo Alto
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larity 100.0%;
Conservative
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
UENCE 21 AA; 2479 MW;
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                                                             RY: USA 94306
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TOPOLOGY: un
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STATE: Ne.
COUNTRY: US:
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US-09-089-595-5
             STREET:
CITY: Pa
STATE: C
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CITY: N
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GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: USE OF IMMUNOCONJUGATES
TITLE OF INVENTION: EFFICACY OF MULTI-STAGE
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                                                                                                                      Score 158; DB 15;
Pred. No. 1.00e-08
0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/577,106
FILING DATE: 22-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/268,129
FILING DATE: 06-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite
                                                US/09/089,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08577106
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                      2810 CN;
PC-DOS
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           SOFTWARE: Wordperfect
RRENT APPLICATION DATA
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
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OPERATING SYSTEM:
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/label= Pep30-2
/note= "Pep30-2 is a synthetically prepared truncated
form of a TNF-alpha analog comprising the human I cell
epitope P30 and flanking portions of human TNF-alpha"
6013 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -alpha molecules, DNI vaccines containing
                                                                                                                                                                                                   Indels
                                                                                                                                                                       Length
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Pred. No. 1.00e-08;
0; Mismatches 0;
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them, and
a or DNA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P60953US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICANT: Martin Roland Jensen
ICANT: Soren Mouritsen
ICANT: Henrik Elsner
ICANT: Iben Dalum
E OF INVENTION: Modified huma
E OF INVENTION: encoding them
E OF INVENTION: TNF-alpha or
                                                                                                                                                                                                                                                                                                                                                                                                                                      38, Application US/09060294 INFORMATION:
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TNF-alpha
42
                                                                                                                                                                                                                                                                                                                 STANDARD;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 31 aming acid;
                                                                                                                                 MW;
                                                                                                                                                               100.0%;
Similarity 100.0%;
21; Conservative
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NO
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                                        NAME/KEY: Peptide
LOCATION: 1..31
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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ADDRESSEE: Farmaceut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Denmark ZIP: DK-2720
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acid
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ORIGINAL SOURCE:
ORGANISM: HOMO
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MOLECULE TYPE:
HYPOTHETICAL: N
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IS-09-060-294-38
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APPLICANT:
APPLICANT:
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GENERAL
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Pred. No. 1.00e-08
0; Mismatches (
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ER: P60953US1
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US/09/060,294
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APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P60953U
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-666
TELEPHONE: (202) 393-5350
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DOS
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060
FILING DATE: 15-APR-1998
                                                                                                                                2920 CN;
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APPLICANT: Soren Mouritsen
APPLICANT: Henrik Elsner
APPLICANT: Iben Dalum
TITLE OF INVENTION: Modified
TITLE OF INVENTION: encoding
TITLE OF INVENTION: TNF-alph
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                        ^{\circ}
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino actrine 
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Indertoften 10
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                                                                  22 amino acids
amino acid
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TOPOLOGY: linear
ICE 22 AA; 2582 MW;
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larity 100.0%;
Conservative
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STRANDEDNESS:
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HYPOTHETICAL: NO
FRAGMENT TYPE: i
ORIGINAL SOURCE:
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es 21; Conse
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US-09-060-294-39
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                     TELEX: INFORMATION
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Peptide

NAME/KEY:

said modified

DNA

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/label= Pep30-5
/note= "Pep30-5 is a synthetically prepared truncated
form of a TNF-alpha analog comprising the human T cell
epitope P30 and flanking portions of human TNF-alpha"
5343 CN;
                                                                                                                                                                                                                                                                                                            said modified
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                                                                                   Gaps
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                                                                                    Indels
                                                               Length
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                                                                 2.08
                                                               Score 158; DB 22
Pred. No. 1.00e-0
0; Mismatches
                                                                                                                                                                 37
                                                                                                                                                                                                                                                                                                                                                                     CITY: Vanloese
COUNTRY: Denmark
ZIP: DK-2720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REGISTRATION NUMBER: 24,514
REGISTRATION NUMBER: 24,514
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R: P60953US1
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                                                                                                                                                                                                                                          Sequence 40, Application US/09060294
GENERAL INFORMATION:
APPLICANT: Martin Roland Jensen
APPLICANT: Soren Mouritsen
APPLICANT: Henrik Elsner
APPLICANT: Iben Dalum
TITLE OF INVENTION: Modified human
TITLE OF INVENTION: encoding them,
TITLE OF INVENTION: TNF-alpha or D
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TNF-alpha (
42
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TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
FORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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3: peptide
                                                                                                                                                                   STANDARD
                                                                                                         26
                                                                                                                           21
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                                                                  100.0%;
larity 100.0%;
Conservative
                                                                                                        FUNFTVSFWLRVPKVSASHLE
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        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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ORIGINAL SOURCE:
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                                                                           Similarity 21; Conserv
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ID US-09-060-294-40
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AC XXXXXX
DT
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                          /label= Pep30-1
/note= "Pep30-1 is a synthetically prepared
form of a TNF-alpha analog comprising human
epitope P30 and flanking portions of human
                                                                                                                                                                                                                                                                                                                               said
                                                                                                      Gaps
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                                                                                  e 158; DB 22;
.. No. 1.00e-08;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                          Laboratorium
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APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3ER: 24,514
NUMBER: P60953US1
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                                                                                  Score 158;
Pred. No. 1
0; Mismat
                                                                                                                                                                                                                                                              42, Application US/09060294 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT - D. Douglas NAME: Price, D. Douglas 24,514 REGISTRATION NUMBER: 24,514 REFERENCE/DOCKET NUMBER: P609 TELECOMMUNICATION INFORMATION: (202) 638-6666 - TELECOMMUNES: (202) 638-6666
                                                                                                                                                                                                                                           Application US/09060294
                                                                  CN;
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                                                        epitope; 4576 CN
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Soren Mouritsen
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
NO
                                                                                                                                                                                                                                                                                                     Henrik Elsner
Iben Dalum
                                                                                                                            26
                                                                                                                                             21
                                                                                                                                                                                                                                                                                  APPLICANT: Martin Roland APPLICANT: Soren Mourits APPLICANT: Henrik Elsner APPLICANT: Henrik Elsner TITLE OF INVENTION: encortitle OF INVENTION: TNF-NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 638-
202) 393-53
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                    Indertoften
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
1..31
                                                                                     100.0%;
100.0%;
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                                                                                                                                    3576 MW;
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o acid
                  LOCATION: 1..31
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Denmark ZIP: DK-2720
                                                                                                                                                                                                                                                                                                                                                                                     STREET: Indertocity (CITY: Vanloese
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amino
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FRAGMENT TYPE:
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                                                                                                Similarity 21; Conse
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LOCATION:
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ORGANISM:
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ID US-09-060-294
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      a TNF-alpha analog comprising the P80 and flanking portions of human
                                                                        Gaps
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.00e-08;
0;
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                                                Score 158; DB 22;
Pred. No. 1.00e-08;
0; Mismatches 0
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Pred. No. 1.00e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/161,889
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible

COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31,259
IR: 0222.002
                                                                                                                                                                                                             Jevence 64, Application US/08161889
GENERAL INFORMATION:
APPLICANT: Geysen, H. Maric
APPLICANT: Rodda
                                                                                                                                                             PRI
                  epitope P3 5344 CN;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
FORMATION FOR SEQ ID NO: 64:
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St.
       form
                                                                                                                                                            STANDARD;
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SEQUENCE CHARACTERISTICS:
LENGIH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Green, Grant D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                   SSEE: Grant D. (T: 4560 Horton)
Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide 3694 MW; (
    INFORMATION: f
INFORMATION: e
31 AA; 3660 MW;
                                               100.0%;
larity 100.0%;
Conservative
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Similarity 100.0%;
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                                                           Similarity
21; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                           31 AA;
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STREET: 45
CITY: Emer
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     OTHER
OTHER
SEQUENCE 3.
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                                                Query Match
Best Local
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Best Local
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               an T cell
?-alpha"
  /note= "Pep30-3 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T celepitope P30 and flanking portions of human TNF-alpha" 6555 CN;
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                                                       DB 22;
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                                                                   No. 1.00e Mismatches
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APPLICATION NUMBER: US/09/060,294

FILING DATE: 15-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/044,187

FILING DATE: 24-APR-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Pep30-4
/note= "Pep30-4
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:R: P60953US1
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                       Score 158;
Pred. No. 1
                                                                                                                                                                                                                                                       US/09060294
                                                                                                                                                                                                                                                                          Martin Roland Jensen
Soren Mouritsen
Henrik Elsner
Iben Dalum
                                                                                                                                                                                                                                 41, Application US/09060294
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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TELECOMMUNICATION INFORMATION:
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(202) 393-5350
R SEQ ID NO: 41
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LENGTH: 31 amino acide
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Similarity 100.0%;
21; Conservative
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REGISTRATION NUMBER:
REFERENCE/DOCKET NUM
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INFORMATION:
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APPLICANT: Henrik El
APPLICANT: Iben Dalu
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
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ORIGINAL SOURCE:
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ZIP: DK-2720
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TELEFAX: (2
INFORMATION FOR
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OPERATING (
SOFTWARE:
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LOCATION:
OTHER INFO
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GENERAL
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Immunogenic LHRH peptide constructs
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Mismatches 0;
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 treatment
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                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/229,275

FILING DATE: 13-APR-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, M L

REGISTRATION NUMBER: 34,045

REFERENCE/DOCKET NUMBER: 2003Z

TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                      I: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application PC/TUS9404832A
 for
vaccines for
infertility
53
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Pred.
0; M
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                                     ADDRESSEE: M. Lisa Wilson STREET: 25 Davids Drive
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                          6283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application FC/10
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunc
TITLE OF INVENTION: and SY
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                              TELEPHONE: (516)273-2828
TELEFAX: (516)273-1717
FORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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acids
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3789 MW: 6
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COMPODERATING SYSTEM: PC
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larity 100.0%;
Conservative
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TITLE OF INVENTION: VETITLE OF INVENTION: 11 NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS
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n City
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nino acid
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NY
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NY
                                             STREET: 25 DCITY: Hauppa
STATE: NY
COUNTRY: US
ZIP: 11788
                                                                                                                                                                                                                                                                            amino
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nes 21; Conse
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ID PCT-US94-04832A-14
                                                                                                                                                                                                                                                                                                         32 AA;
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                                                                                                               COMPUTER:
OPERATING
SOFTWARE:
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STREET: 4
CITY: Gar
STATE: NY
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TYPE: am
TOPOLOGY:
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31
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                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/161,889A
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
                                                                                                                                                                                                                                                                                                                                               .002
                                                                                                                Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 1
                                                                                                                                                                                                           TYPE: Floppy disk
SR: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158;
Pred. No. 1
0; Mismat
                                                                         Sequence 64, Application US/08161889A
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitop
NUMBER OF SEQUENCES: 74
                                                        Application US/08161889A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/0822927
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic
                                                                                                                                                                                                                                                                                                                                              1222
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Z
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                            Green
St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6041
 STANDARD;
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STREET: 4550 Horton
CITY: Emeryville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
Similarity 100.0%;
21; Conservative
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STRANDEDNESS: sing
TOPOLOGY: Linear
MOLECULE TYPE: pept:
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COMPUTER: IBM PC
OPERATING SYSTEM:
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3694
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US-08-161-889A-64
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US-08-229-275-14
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And A Helper T-Cell Epitope For Treatment
And Induction Of Infertility
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1.00e-08;
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,320A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                     4
                   e 158; DB 4
. No. 1.00e-
Mismatches
                                                                                                                                      PRT;
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Pred. No. 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,351
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/229,275
FILING DATE: 14-APR-1994
APPLICATION NUMBER: 08/229,275
FILING DATE: 14-APR-1994
APPLICATION NUMBER: 08/057,166
FILING DATE: 27-APR-1993
                                                                                                                                                                                                                                  14, Application US/08488320A INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                           Application US/08488320A
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS AND SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                             1: 345 PARK AVENUE
NEW YORK
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Pred.
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Zamb, Timothy
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larity 100.0%;
Conservative
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REGISTRATION NUMBER:
                     100.0%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                           Ladd, Anna
MW;
                                                                               FINITUSEWLEVPKVSASHLE
                                                                                                                                                                                                                                    Sequence 14, Application GENERAL INFORMATION:
APPLICANT: Ladd, Anna APPLICANT: Wang, Chan APPLICANT: Zamb, Timo TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF SEQUENCES:
                                                                    FUNFIVSFWLRVPKVSASHLE
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3789
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TOPOLOGY: li
MOLECULE TYPE:
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21; Conser
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US-08-488-320A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE INFORMATION.
GENERAL INFORMATION.
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: and a Helper T Cell Epit
TITLE OF INVENTION: Cancer and Induction of
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: M. Lisa Wilson, United Biomedi
STREET: 25 Davids Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version
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Pred. No. 1.00e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERAIING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vecurrent APPLICATION DATA: APPLICATION NUMBER: US/08/057,166 FILING DATE: 19930427 CLASSIFICATION: 424
 APPLICATION NUMBER: PCT/US94/04832A FILING DAIE: 13-APR-1994 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     PRI;
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COUNTRY: U.L.
ZIP: 11788
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMPUTER: IBM PC COMPATIBLE
TAMPUTER: ISM PC COMPATIBLE
TAMPUTER: TAMPUTER: PC-DOS/MS-D
TAMPUTER: TAMPUTER: PC-DOS/MS-D
TAMPUTER: TAMPUTER: PC-DOS/MS-D
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                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08057166
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                                                              REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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(516)273-1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wilson, M. Lisa
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGIH: 32 amino acids
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                                                                                                                                              amino acids
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3789 MW: 6
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Similarity 100.0%;
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CITY: Hauppauge
STATE: NY
COUNTRY: U.S.A.
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US-08-057-166-14
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TYPE: ami
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them, and vaccines containing
or DNA
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                                                                                                                                                              ADDRESSEE: Farmaceutisk Laboratorium Ferring STREET: Indertoften 10
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                                                                                                                                                                                                                                 MEDIUM 1112...
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P60953US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-666
TELEFAX: (202) 638-666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TVPE: amino acid
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1.00e-08;
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Pred. No. 1.00e-
0; Mismatches
                    Sequence 12, Application US/09060294
GENERAL INFORMATION:
APPLICANT: Martin Roland Jensen
APPLICANT: Soren Mouritsen
APPLICANT: Henrik Elsner
APPLICANT: Henrik Elsner
APPLICANT: Iben Dalum
TITLE OF INVENTION: Modified human
TITLE OF INVENTION: encoding them,
TITLE OF INVENTION: TNF-alpha or DI
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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17648 MW; 130661 CN;
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GENERAL INFORMATION:
APPLICANT: Martin Roland Jensen
APPLICANT: Soren Mouritsen
APPLICANT: Henrik Elsner
APPLICANT: Iben Dalum
TITLE OF INVENTION: Modified human
TITLE OF INVENTION: encoding them,
TITLE OF INVENTION: TNF-alpha or Di
NUMBER OF SEQUENCES: 42
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   Application US/09060294
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                                                                                                                                                                                                COUNTRY: Denmark
ZIP: DK-2720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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100.0%;
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CORRESPONDENCE ADDRESS:
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encoding them, and
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Pred. No. 1.00e-
0; Mismatches
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ZIP: DK-2720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
                                                                                                                                                                                                                                                                              DNA
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R: P60953US1
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L INFORMATION:
ICANT: Martin Roland Jensen
ICANT: Soren Mouritsen
ICANT: Henrik Elsner
ICANT: Iben Dalum
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TNF-alpha
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REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P(
ILECOMMUNICATION INFORMATION
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 638-6666
202) 393-5350
(SEQ ID NO: 16:
                                                                           STANDARD;
   23
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LENGTH: 158 amino acids
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17696 MW;
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Farmaceut
STREET: Indertoften
 FNNFTVSFWLRVPKVSASHLE
             Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative
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                                                                                                                                                   Application
                                                                                                                                                                                              APPLICANT: Martin Reapplicant: Soren MoraPPLICANT: Henrik E. APPLICANT: Iben Dalitite OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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acid
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TYPE:
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9-060-294-
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CITY: V
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GENERAL
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TELEPHONE: (202) 638-666
IELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
                                                                                                            linear
                                                                                                   TYPE: amino TOPOLOGY: lin MOLECULE TYPE: UENCE 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SOFTWARE:
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US-09-060-294-18
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TYPE: a
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                                                                         (EPO)
                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,294
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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Pred. No. 1.00e-
0; Mismatches
    Laboratorium
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ER: P60953US1
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15-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                           Martin Roland Jensen
Soren Mouritsen
Henrik Elsner
Iben Dalum
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TNF-alpha (
42
                                                                                                                                     NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 638-5666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 14
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   Farmaceutisk
ertoften 10
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17598 MW;
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MEDIUM TYPE: Floppy
                                         COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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ADDRESSEE: Farmaceut
STREET: Indertoften
CITY: Vanloese
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application
GENERAL INFORMATION:
APPLICANT: Martin Rc
APPLICANT: Soren Mou
APPLICANT: Henrik El
APPLICANT: Iben Dalu
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                    amino
acid
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                          COUNTRY: Deni
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SEQUENCE 158 AA;
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US-09-060-294-20
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STREET: Indertoften 10
CITY: Vanloese
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. No. 1.00e-08;
Mismatches 0
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Price, D. Douglas
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P60953US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24,514
R: P60953US1
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FILING DATE: 15-APR-1998
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Pred. No. 1
0; Mismat
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,187
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09060294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jensen
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TNF-alpha 42
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REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Martin Roland Jen
APPLICANT: Soren Mouritsen
APPLICANT: Henrik Elsner
APPLICANT: Iben Dalum
TITLE OF INVENTION: Modified
TITLE OF INVENTION: encoding
TITLE OF INVENTION: TNF-alph
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
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17528 MW;
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ZIP: DK-2720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Similarity 100.0%;
21; Conservative
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GENERAL INFORMATION:
CHERAL INFORMATION:
CHITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT AND TEXT
CHILE REFERENCE: 216-380P
CHILE REFERENCE: 216-380P
CURRENT APPLICATION NUMBER: US/08/913,880
CURRENT FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 9
COFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1315
CHITLE OF INVENTIONAL TETANUS
COFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
CHITLE OF INVENTIONAL TETANUS
CHITLE OF INVENTIONAL TETANUS
COFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
CHITLE OF INVENTIONAL TETANUS
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Pred. No. 1.00e-08
0; Mismatches
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Pred. No. 1.00e-08;
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17566 MW;
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Best Local Similarity 100.0%;
Matches 21; Conservative
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Best Local Similarity 100.0%;
Matches 21; Conservative
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro-
SEQUENCE 158 AA; 1756
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Collins, Biocomputing Research 998 University of Edinburgh, U. rights by Oxford Molecular Ltd Release 3.1A John F. Co] Copyright (c) 1993-1998 Distribution rig

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Tabular

>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Φ Title: Description: Perfect Score Sequence:

PAM 150 Gap 15 Scoring table:

50406085 residues 411786 seqs, Searched

Post-processing

summaries Minimum Match 100% Listing first 1000 sum Maximum DB seq length

Database

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92 18:U93 19:NEWP 20:NEWU6 21:NEWU8 22:NEWU9

0.300 scale Variance 74.265; Mean 22.277; Statistics:

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed; derived by analysis of the total score distribution. Pred. No. score greand is de

SUMMARIES

158 100.0 158 100.0 158 100.0 158 100.0 158 100.0 158 100.0 158 100.0 158 100.0	 - 		Description	Drad No
588 100. 588 100. 588 100. 588 100. 588 100. 588 100.				. ;
588 100. 588 100. 588 100. 588 100. 588 100. 588 100.	4	US-08-432-	Sequence 3, Applicatio	1.00e-08
58 100. 58 100. 58 100. 58 100. 58 100. 58 100.	21 14	US-08-945-	3, Applicati	- 1
58 100. 58 100. 58 100. 58 100. 58 100. 58 100.		US-07-678-	plicati	0-
58 100. 58 100. 58 100. 58 100. 58 100. 58 100.	1 1	US-09-049-	2, Applicati	.00e-0
58 100. 58 100. 58 100. 58 100. 58 100.	1 1	US-09-171-	10, Applicat	e-0
58 100. 58 100. 58 100. 58 100. 58 100.	⊢	US-08-724-	5, Applicati	e-0
58 100. 58 100. 58 100. 58 100.	⊣	US-08-406-	4, Applicati	.00e-0
58 100. 58 100. 58 100.	21 5	US-08-161-	ce 66, Appli	.00e-0
58 100. 58 100.	\leftarrow	US-08-432-	Applicati	0
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ALIGNMENTS

AA 21 PRT; STANDARD; US-08-432-483A-3 RESULT ID US

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                                                       TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner of STREET BANNER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panina-Bordignon, P., et al.
Universally immunogenic T cell
epitopes: promiscuous binding to human MHC
promiscuous recognition by T cells
European Journal of Immunology
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                                                                                                                                                                                                                                                                                                               NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179(TCS-9517)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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1.00e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    toxoid
                                                                                                                                                                                                MEDIUM L. COMPUTER: IBM PC COMPUTER: BM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-LC-SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/432,483A
FILING DATE: 1-May-1995
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
NAME: Leon R. Yankwich
TTON NUMBER: 30,237
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                                                                                                                                                                                                                                                                                                                                                                                                                                    tetanus
epitope.
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MEDIUM TYPE: diskette
COMPUTER: IBM PC COMPAtible
ODFRATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1
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                                                                                                                                   Banner & Witcoff, L
South Wacker Drive
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                                                Application US/08432483A
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PUBLICATION INFORMATION:
AUTHORS: Panina-Bordi
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                                                                Sequence 3, Application
GENERAL INFORMATION:
APPLICANT: Rittersha
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19
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DATE: 1989
RELEVANT RESIDUES
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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60606-7407
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: HYPOTHETICAL:
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NAME/KEY:
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FEATURE:
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TITLE: P
JOURNAL:
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TYPE: a
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US-08-945-289
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                                                Sequence
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IMMUNOGENIC COMPOUNDS, THE PROCESS FOR THEIR SYNTHESIS AND THEIR USE IN THE PREPARATION ANTIMALARIA VACCINES
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GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Leclerc, Claude
APPLICANT: Lo-Man, Richard
TITLE OF INVENTION: Mutiple antigen alycopeptide carbohydrate,
TITLE OF INVENTION: comprising the same and use thereof
FILE REFERENCE: 102.166A
CURRENT APPLICATION NUMBER: US/09/049,847
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/041,726
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Mismatches
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01 Apr 1991
N: 424
                                                                                                                                      the Americas
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                                                                                                                                                                                                inch,
                                                                                                                                                                   of America
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 158;
Pred. No. 1
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 incl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                       APPLICANT: Elisabetta BIANCHI
APPLICANT: Giampietro CORRADIN
TITLE OF INVENTION: IMMUNOGENIC (
TITLE OF INVENTION: THEIR SYNTHES
TITLE OF INVENTION: ANTIMALARIA V
NUMBER OF SEQUENCES: 7
CORRESPONDENCE APPLICATION
                            US/07678684B
                                                                                                                                                                                                                                                                            02 Apr 1990
N: 424
         US/07678684B
                                                                                                                                                                                                                           SOFTWARE: IBM DISPLAY WRITER CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/678
                                                                                                                                                                                                                                                                                                                                                                                                         CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09049847
                                                                                                                                                                                                                                                                                              FILING DATE: 02 Apr 1990
CLASSIFICATION: 424
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          (212) 827-3000
(212) 840-6702
                                                                                                                                                                                                                                                                                                                                                          1:
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                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SHEA & GOULD
STREET: 1251 Avenue of th
CITY: New York
STATE: New York
COUNTRY: United States of
ZIP: 10020-1193
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                                                                                                                                                                                                                                                                                                                                                                           acids
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CHARACTERISTICS
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
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larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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amino acid
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                           1, Application:
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21; Conser
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TELEFAX:
                          Sequence 1, App
GENERAL INFORMAPPLICANT:
APPLICANT:
APPLICANT:
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                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
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Pred. No. 1
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Universally immunogenic
European Journal of In
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1,1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:
                                                                                                                                                                                                                                                        US/08/945,
r 17, 1997
                                                         US/08945289
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E: Floppy disk
IBM PC compatible
                                      US/08945289
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/CFILING DATE: October 17, CLASSIFICATION: 514
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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Similarity 100.0%;
21; Conservative
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DATE: 1989
RELEVANT RESIDUES: NCE 21 AA; 2479 M
                                                        3, Application INFORMATION:
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3Y: linear
                                     Application
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HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
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JOURNAL: Eu
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US-07-678-684B-1
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ISSUE:
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i, Donata; Jongeneel, Victor; Car.
Reed, Daryl
MAGE-10 ENCODING cDNA, The Tar.
Rejection Antigen Precuros Maribodies Specific To The Maribodies Specific To The Maribodies Thereof
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Pred. No. 1.00e-08,
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    Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,774B
FILING DATE: 03-October-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      5457
                                                                          PRT;
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                                                                                                                                                 5, Application US/08724774B
INFORMATION:
ANT: Rimoldi, Donata; Jong
ANT: Pierre; Cerrottini, J
                                                                                                                               Application US/08724774B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08406916B
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2810 CN;
                                                                                                                                                                                                                                                                                                                    3.5
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TELEFAX: (212) 838-3884
FORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
   0
                                                                                                                                                                                                                                                   SEE: Felfe & Lynch: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                      PC-DOS
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                     21
                                                                                                                                              Sequence 5, Application US/0 GENERAL INFORMATION:
APPLICANT: Rimoldi, Dona APPLICANT: Pierre; Cerro APPLICANT: Stefan; Reed, TITLE OF INVENTION: Reje TITLE OF INVENTION: Anti TITLE OF INVENTION: USES NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
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21; Conservative
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OPERATING SYSTEM:
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: USA
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CITY: New Y
STATE: New
COUNTRY: US
ZIP: 10022
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                                                                        US-08-724-774B-5
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SEQUENCE
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Pred. No. 1.00e-08;
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                                                                               Score 158; DB 15;
Pred. No. 1.00e-08
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.93)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yank****
REGISTRANT
                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (21.02)
                                                                                                                                                                                                                                                                                                        street, Suite 2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414.1
                                                                                                                                                                                                                                                                                                                                                             ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
WordPerfect 6.1
                                                                                                                                                                                                                                                Sequence 10, Application US/09171969
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED
NUMBER OF SEQUENCES: 10
                                                                                                                                                                            PRT
                                                                                                                                                                                                                                 US/09171969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS
INFORMATION FOR SEQ ID NO: 10:
                                                               CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĊŊ;
EARLIER FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                   Massachusetts
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100.0%;
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                                                                                1 100.0%;
Similarity 100.0%;
21; Conservative
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State 9
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AIP: 02109-1807

COMPUTER READABLE FO

MEDIUM TYPE: Flop!

COMPUTER: IBM PC (
OPERATING SYSTEM:
SOFTWARE: WORTH
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AA;
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STREET: 75
CITY: BOST
STATE: Mas
COUNTRY: U
ZIP: 02109
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TH: 21
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                                                    ORGANISM: (SEQUENCE 21
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FEATURE:
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ID US-09-171
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ATTORNEY/AGENT INFORMATION:
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6 DX 33
                                   ANTIGENIC
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                                                          ADDRESSEE: MILLARD, SIDNEY W.
STREET: 7632 SLATE RIDGE BOJLEVARD
CITY: REYNOLDSBURG
STATE: OHIO
COUNTRY: USA
ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44
COMPUTER: IBM PS/2 COMPATIBLE 486 DX
OPERATING SYSTEM: MS DOS 6.2
                                                                                                                                                  5.1
                                                                                                                                                                                                                                       (L_{k})
                                                                                                                                                                                         APPLICATION NUMBER: PCT/US92/08370
FILING DATE: 30 SEP 1992
ATTORNEY/AGENT INFORMATION:
NAME: KREMBLAS, FRANCIS T., JR.
REGISTRATION NUMBER: 22,773
REFERENCE/DOCKET NUMBER: URF 2 056
                                                                                                                                      OPERATING SYSTEM: MS DOS 6.2
SOFTWARE: WORDPERFECT FOR MS DOS 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,916B
FILING DATE: 27 MAR 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             l epitope
CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stuart J.: T-Cell Epitopes
5: 74
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GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
                                   AND
         US/08406916B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08161889A
                                                                                                                                                                                                                 NAME: KREMBLAS, --- 22,773
REGISTRATION NUMBER: 22,773
REFERENCE/DOCKET NUMBER: URF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 575 2100
TELEFAX: (614) 575 2149
TELEFAX: (614) 575 2149
      equence 4, Application US/0840691
SENERAL INFORMATION:
APPLICANT: STEVENS, VERNON C.
TITLE OF INVENTION: VACCINES A
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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2810 C
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St.
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LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TOPOLOGY:
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APPLICANT: Rodda, Stuar
TITLE OF INVENTION: T-C
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant
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Emeryville
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21; Conservative
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21 AA; 2479 MW;
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DESCRIPTION:
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ID US-08-161-889A-66
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CITY: E
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OTHER
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GENERAL
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GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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Pred. No. 1.00e-08;
0; Mismatches 0
                                                                                              UPERATING SISIEM: FC-DUS/MS DUS

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/161,889A

FILING DATE: 02-DEC-1993

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION OF 02-092

FILING DATE: 02-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Green, Grant D.

REGISTRATION NUMBER: 31,259

REFERENCE/DOCKET NUMBER: 0222.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-601-2706

TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE 21 AA; 2479 MW; 2810 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
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STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
                                DABLE FORM.
PE: Floppy disk
IBM PC compatible
""CTEM: PC-DOS/MS-DOS"
""CTEM: PC-DOS/MS-DOS"
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
Similarity 100.0%;
21; Conservative
                                                                                        OPERATING SYSTEM: SOFTWARE: Patent
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                                       COMPUTER READABLE MEDIUM TYPE: F]
COUNTRY: US
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Pred. No. 1.00e-08
0; Mismatches
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NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Associates
venue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
TYPE: TOWN PC COMPATIBLE
TYPE: Floppy disk
COMPUTER: TOWN PC COMPATIBLE
TYPE: TYPE: TOWN PC COMPATIBLE
TYPE: TYPE: TOWN PC COMPATIBLE
TYPE: TOWN PC COMPATIBLE
TYPE: TOWN PC C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08245507
GENERAL INFORMATION:
APPLICANT: Houston, Michael
APPLICANT: Zhou, Nian
APPLICANT: Kay, Cyril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08245507
                                                                                                                                                                                                       2810 CN;
                   REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kay, Cyril
APPLICANT: Hodges, Robert
APPLICANT: Cachia, Paul
APPLICANT: Irvin, Randall
TITLE OF INVENTION: Heteroc
TITLE OF INVENTION: Compos:
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay, Cyril
Hodges, Robert
Cachia, Paul
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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ADDRESSEE: Dehlinger & STREET: 350 Cambridge A CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306
                                                                                                                    1: 21 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                            21
                                                                                                               LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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LENGTH: 21 amino acids
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21; Conservative
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US-08-245-507-14
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                                                                                                                                                                                                                                                                 Universally immunogenic T cell epitopes: promiscuous binding to human MHC promiscuous recognition by T cells
European Journal of Immunology
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R. Yankwich
N NUMBER: 30,237
- TIMBER: 95,179(ICS-95179)
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ZIP: 94608

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/161,889

TTLING DATE: 02-DEC-1993

TTLING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66, Application US/08161889
GENERAL INFORMATION:
APPLICANI: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                   tetanus
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Pred. No. 1
0; Mismat
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Emeryville
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2810
                                                                                                                                                                                                                  acid
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NN FOR SEQ ID NO:
CHARACTERISTICS:
                                           REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                          NAME/KEY: 21-amino aci
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Panina-Bordio
                                                                                                                                               peptide
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CLASSIFICATION: 435
PRIOR APPLICATION DAIA:
APPLICATION NUMBER:
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larity 100.0%;
Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                         European
19
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                                                                                              : 21 amino amino
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AA; 2479 M
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1989
                                                                                                                             inear
             NAME: Leon F
REGISTRATION
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                                                                                                                                          MOLECULE TYPE: HYPOTHETICAL:
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US-08-161-889-66
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                                                                                                           TYPE: an TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                 JOURNAL:
VOLUME:
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                                                           INFORMATION
SEQUENCE C
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TITLE:
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PAGES:
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CITY:
STATE:
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FEATURE:
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Matches 2
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e; Cerrottini, Jean-Charles; Carrel,
n; Reed, Daryl
N: MAGE-10 ENCODING CDNA, The Tumor
N: Rejection Antigen Precuros Mage-10,
N: Antibodies Specific To The Molecule, an
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Pred. No. 1.00e-08;
0; Mismatches 0;
                                                                     Score 158; DB 6; Li
Pred. No. 1.00e-08;
0; Mismatches 0;
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STRTE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144
COMPUTER: BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,595
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: LUD 5457
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LAWRER
                                                                                                                                                                                                                 PRT;
                            r antigen,
2810 CN;
                                                                                                                                                                                                                                                                                                                             US/09089595
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APPLICANT: Rimoldi, Done
APPLICANT: Stefan; Reed,
TITLE OF INVENTION: Reje
TITLE OF INVENTION: Anti
TITLE OF INVENTION: Anti
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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GY: linear
1 AA; 2479 MW;
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larity 100.0%;
Conservative
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
SEQUENCE 21 AA; 2479 MW;
                                                                     100.0%;
Similarity 100.0%;
21; Conservative
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21; Conser
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TOPOLOGY:
SEQUENCE 21 AA
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ID US-09-089-595-5
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 1.55 Seconds 137.199 Million cell updates/sec Tue Aug 17 16:11:13 1999; Run on:

not generated. output Tabular

>US-09-049-847-2 (1-21) from US09049847.pep 158 1 FNNFTVSFWLRVPKVSASHLE 21 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 table: Scoring

106580 segs, 10152877 residues

Searched:

Post-processing:

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Minimum Match 0% Listing first 45 summaries

scale 0.286 Variance 71.502; Mean 20.415; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ж			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Descripti	Pred. No.
	15	0.0	<u>.</u> 2		 S-08-460	equence 8, Applicati	750-0
7	N	00.		Н	8-01-6	equence 1. Applicat	0.000
m	Ŋ	00.		7	S-08-661	equence 12, Applicat	0.0 0.0 0.0 0.0 0.0 0.0 0.0
4	Ŋ	00.		m	CI-US93~	equence 66, Applicat	250-0
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9	S	00.		7	5-08-488	equence 14, Applicat	250-0
7	Ŋ	00.		7	5-08-44	equence 14, Applicat	250-0
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10	158		452	⊢ i	US-07-618-	quence 2, Applicati	0-0
	ហ	00.	S	Н	S - 08 - 28	equence 2, Applicati	.25e-0
	ıΩ	00.	S	H	S-08-11	equence 8, Applicat	.25e-0
	Ŋ	00	ᅼ	7	S-08-668	equence 5, Applicati	.25e-0
	S	9		C)	CT-US95	equence 8, Applicati	.50e-0
	S	9		7	S - 08 - 488	equence 5, Applicat	.50e-0
	S)	છ		7	S-08-44	equence 5, Applicati	.50e-0
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	$^{\circ}$	<u>о</u>		Н	S - 07 - 610	equence 3, Applicati	.04e-0
	\dashv	ო		7	-78	quence 43, Applica	.23e-0
	\dashv	ო		Н	19-10-S	equence 6, Applicati	.23e-0
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	\dashv			7	S-08-78	equence 44, Applica	01e

13 1 US-07-610- Sequence 5, Applicatio 7.54e-03 438 1 US-08-480- Sequence 23, Applicati 6.34e-02 452 1 US-08-480- Sequence 26, Applicati 6.34e-02 1296 1 US-08-480- Sequence 28, Applicati 6.34e-02 785 1 US-08-946- Sequence 4, Applicatio 1.17e+01 510 1 US-08-946- Sequence 1, Applicatio 1.17e+01 510 1 US-08-16- Sequence 1, Applicatio 1.342e+01 297 2 US-08-489- Sequence 16, Applicatio 3.42e+01 297 2 US-08-461- Sequence 3, Applicatio 3.42e+01 297 2 US-08-808- Sequence 5, Applicatio 6.44e+01 423 2 US-08-448- Sequence 5, Applicatio 9.77e+01 113 2 US-08-477- Sequence 5, Applicatio 9.77e+01 294 1 US-08-634- Sequence 6, Applicatio 9.77e+01 256 3 PCT-US95-0 Sequence 6, Applicatio 1.20e+02 256 3 PCT-US95-0 Sequence 157, Applicatio 1.20e+02	ALIG] STANDARD; stion US/0846(ation US/0846(ation US/0846(ation)) ation US/0846(ation) ation US/0846(ation) ION: Appropriate Superior Averand ADDRESS: alfee, Haltersuperior Averand ADDRESS: alfee, Haltersuperior Averand INFORM: Floppy disk M PC compatible Superior Averand INFORM: ADDRESS: alfee, Haltersuperior Averand Superior Averand ADDRESS: alfee, Haltersuperior Averand ADDRESS: alfee, Haltersuperior Averand Superior Averand ADDRESS: alfee, Haltersuperior Averand Superior Averand Superior Averand ADDRESS: alfee, Haltersuperior ADDRESS: ANDRESS: ANDRESS: ANDRESS: ALIGORY ANDRE	479 MW
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No. 3.25e-09;
Mismatches 0;
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                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ltd
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                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                 MXI-043CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Lta
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 158;
Pred. No. 3
0; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9311703
                                                                                                                                                                      Suite
                                              US/08661052
                                                                                                             Somasundaram
                                                                                                                                                                                                                                                                                                                                         NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                            & COCKFIELD
                           Application US/08661052
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internal
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Joel Goldstein
Robert Graziano
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                                                                                                                                                                      Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & CC
STREET: 60 State Street
                                                                                                                                                                                        : Massachusetts
RY: USA
02109-1875
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                                              Sequence 12, Application
Patent No. 5837243
GENERAL INFORMATION:
                                                                            APPLICANT: Yashwant
APPLICANT: Joel Gold
APPLICANT: Robert Gr
APPLICANT: Chezian S
TITLE OF INVENTION:
                                                                                                            Chezian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 21; Conser
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FRAGMENT TYPE:
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                                                                                                                                                                                         STATE: MCOUNTRY: ZIP: 021
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                                                                                                                                                                                        Sequence 1, Application US/07610525
Patent No. 5196512
GENERAL INFORMATION:
APPLICANT: BIANCHI Eisabetta
APPLICANT: DESSI Antonello
APPLICANT: CORRADIN Giampietro
TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS
TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC OTITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHEA & GOULD
STREET: 1251 AVENUE OF THE AMERICAS
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. No. 3.25e-09;
Mismatches 0;
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Pred. No. 3.25e-09
0; Mismatches
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                                                                                                             21
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/610,525
FILING DATE: 19901108
CLASSIFICATION: 424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-827-3000
TELEFAX: 212-840-6702
TELEX: 423973
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             STREET: 1251 AVENUE OF IND CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES
ZIP: 10020-1193
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/07/610,525
19901108
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       Score 158;
Pred. No. 3
0; Mismat
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2479 MW; 2810 CN;
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21; Conservative
          100.0%;
larity 100.0%;
Conservative
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AMINO ACID
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                                                                                                                                                                       Application
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1251 AV
FW YORK
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MOLECULE TYPE:
HYPOTHETICAL: 1
FRAGMENT TYPE:
UENCE 21 AA; 2
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                    Similarity 21; Conser
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ID US-08-661-052-12
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TYPE: A
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US-07-610-525
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MBER: US 08/057,166
27-APR-1992
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 27-APR-1
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                                                                                                                                                      100.0%;
100.0%;
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                                                                                                                                                                                              FILING DATE: 7-JUN-
CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION NUMBER:
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                               Similarity 21; Conser
                                                                                                                                TYPE:
                                                                                                                                       31 AA;
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                                                                                                                                MOLECULE
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STATE:
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3-08-488-3
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                                                                               Version #1.30B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
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3.25e-09;
                                                                                                                                                                                                                                                                                No. 3.25e Mismatches
                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION OATA:
APPLICATION NUMBER: US 07/984,852
FILING DAIE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-655-3542
THEODEWARTION FOR STO IN NO. 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                  s Pty. Ltd.
Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. L.
TITLE OF INVENTION: T-Cell Epitope,
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
                                                                                                                                                                                                                                                                      Score 158;
Pred. No. 3
0; Mismat
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LENGTH: 21 amin
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larity 100.0%;
Conservative
ADDRESSEE: Grant D.
STREET: 4560 Horton
CITY: Emeryville
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                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                        amino acid
                                USA
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ZIP: 94608
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Best Local Similarity
Matches 21; Conser
                CLLL.
STATE: CA
COUNTRY: US.
The 94608
                                                                                                                                                                                                                        TYPE: amino STRANDEDNESS
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PCT-US93-11703-64
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CITY: E
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and synthetic universal i
114
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ZIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                e 158; DB 3; L.
No. 3.25e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                          31,259
ER: 0222.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRF
TITLE OF INVENTION: and synthetic ur
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                        07/984,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                          158;
No. :
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14-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14, Application US/08488351A
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/984
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                            6041 CN;
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Pred.
0; M
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                                                                                                                                                             TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                  Score 158; DB 2; Le
Pred. No. 3.25e-09;
0; Mismatches C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crawford Mr, Arthur R
REGISTRATION NUMBER: 25,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/618,312A FILING DATE: 19910516 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 8926832.0
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TOPOLOGY: linear
DIECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: 14th Floor
STREET: 2200 Clarendon Boulevard
CITY: Arlington,
                                                                                                                                  PRT;
                                                                                                                                                                                                                   Sequence 4, Applicactory
Patent No. 5389540
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil F
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEFAX: 0101 703 8750400
TELEFAX: 0101 703 5253468
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                    Application US/07618312A
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larity 100.0%;
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21; Conse
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COUNTRY: U.
ZIP: 22201
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SEQUENCE 452
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US-07-618
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Pred. No. 3.25e-09
0; Mismatches
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NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154-0053
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                             29,323
JR: 1151-4146
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08446692
Patent No. 5759551
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LH
TITLE OF INVENTION: and synthetic
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CLASSIFICAL.

ATTORNEY/AGENT INFORM.

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                          STANDARD;
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LENGTH: 32 amino acids
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3789 mm· f
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3789 MW· 6
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Similarity 100.0%
21; Conservative
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10 acid
linear
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SEQUENCE 32 AA;
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MOLECULE TYPE:
SEQUENCE 32 AA;
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INFORMATION FOR
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Makoff Dr, Andrew J Romanos Dr, Michael Clare Dr, Jeffrey J

ey J Neil

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ADDRESSEE: 14th Floor
STREET: 2200 clarendon Boulevard,
CITY: Arlington,
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/618,312A
FILING DATE: 19910516
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
FILING APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Crawford Mr, Arthur R
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 510-51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 0101 703 8750400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                   Application US/07618312A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 0101 703 8750400
TELEFAX: 0101 703 5253468
TELEX: 200797 NIXN UR
INFORMATION FOR SEC ID 100
                                                                                         Sequence 2, Application US/07618:
Patent No. 5389540
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew APPLICANT: Romanos Dr, Michae APPLICANT: Clare Dr, Jeffrey APPLICANT: Fairweather Dr, Nettle OF INVENTION: VACCINES NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 amino acids
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/280,228

FILING DATE: 25-JUL-1994

CLASSIFICATION: 435
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Pred. No. 3.25e-09;
0; Mismatches 0
                                   452
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                                                                                                                                                                                                                                                                          NIXON & VANDERHYE P.C O NO. 5571694th Glebe
                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFLICATION NUMBER: US/UD/200,226
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/618,31:
FILING DATE: 27-NOV-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US 07/618,31
27-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,955
R: 117-163
                                                                                                                                   Sequence 4, Application US/08280228
Patent No. 5571694
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil F
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.(
                                   PRT;
                                                                                                                                                                                                Ą
                                                                                                              Application US/08280228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: (703) 816-4000
(703) 816-4100
00797 NIXN UR
OR SEQ ID NO: 4:
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                                 STANDARD;
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51770 MW;
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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INFORMATION FOR SE
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MOLECULE TYPE:
SEQUENCE 452 AA;
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US-07-618-312A-2
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ID US
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MBER: GB 8926832 28-NOV-1989

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                   Score 158; DB 1; Ler
Pred. No. 3.25e-09;
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protein
51797 MW; 1065526 CN;
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                                                                                                                                                                            Sequence 2, Application US/08280228
                                                               104
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                      100.0%;
| Similarity 100.0%;
21; Conserved
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Pred. No. 3.25e-09,
0; Mismatches
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  tetanus
                                                      Road
                                                                                                                                                                                                                                                 AFFLICATION NUMBER: US 07/77,337
FILING DATE: 29-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00943
FILING DATE: 20-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8914122.0
FILING DATE: 20 June 1989
ATTORNEY/AGENT INFORMATION:
NAME: Mary J. Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/COUNT
                                                                                                                                                                                  COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,786A
FILING DATE: 23-AUG-1993 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,337
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                                         & Vanderhye P.C 5443966th Glebe
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Patent No. 5780024
GENERAL INFORMATION:
APPLICANT: Brown, Robert H.
APPLICANT: Fishman, Paul S.
APPLICANT: Francis, Jonathan W.
APPLICANT: Hosler, Betsy A.
TITLE OF INVENTION: SUPEROXIDE DITITLE OF INVENTION: FRAGMENT C HY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
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REFERENCE/DOCKET NUMBER: 117
TELECOMMUNICATION INFORMATION:
  Expression
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TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 8:
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51784 MW;
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TITLE OF INVENTION: EXNUMBER OF SEQUENCES: 8
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Local Similarity 100.0%;
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                                         ADDRESSEE: N:
STREET: 1100
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US-08-668-381A-
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STATE: V
COUNTRY:
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                                                                                                                                            CITY: Arlington,
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,228
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
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3.25e-09;
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Pred. No. 3.25e-
0; Mismatches
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APPLICATION NUMBER: GB 8926832.0

FILING DATE: 28-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9006097.1

FILING DATE: 17-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mary J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 117-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08110786A
Patent No. 5443966
GENERAL INFORMATION:
APPLICANT: FAIRWEATHER, Neil Fraser
APPLICANT: MAKOFF, Andrew Joseph
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/618,312
FILING DATE: 27-NOV-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1065526 CN;
                                                                                                                          ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 No. 5571694th Glebe
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TELEPHONE: (703) 816-4000
TELEX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
                                                                     Neil
                               Andrew J
Michael
Patent No. 5571694
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Nei.
TITLE OF INVENTION: VACCINES
                                         APPLICANT: Romanos Dr, Michael
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Nei
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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larity 100.0%;
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JENCE 452 AA;
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ID US-08-110-786A-8
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TOPOLOGY:
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3ER: 29,323
NUMBER: 1151-4117
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APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
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14-APR-1994
                                                                                                                                                                                                                                                                                                                  PRT;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                              5, Application US/08488351A
           PRIOR.

APPLICATION.
FILING DATE: 25-C.
CLASSIFICATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TVPE: amino acid
TVPE: amino acide
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N: 424
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APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunc
TITLE OF INVENTION: and sy
NUMBER OF SEQUENCES: 114
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Avenue
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FILING DATE: 14-APR-CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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TOR APPLICATION DATA:
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IOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 7-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Maria
STREET: 345 Park
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application Patent No. 5843446 GENERAL INFORMATION:
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MOLECULE TYPE:
SEQUENCE 22 AA: 3
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STATE: N
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            STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,381A

PTLING DATE: 21-JUN-1996
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ON: Synthetic IgE Membrane ..
ON: Peptide Immunogens for t
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Pred. No. 3.25e-09
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                             NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00786/269001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ER: PCT/US95/13841
-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application PC/TUS9513841
GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Ware APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IGE Matter OF INVENTION: Peptide Immunogenumber OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                  protein
68895 MW; 1991829 CN;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1384.
FILING DATE: 25-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                  FILING DATE: 21-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,473
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
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  Street
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  Franklin
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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21; Conservative
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INFORMATION FOR SE
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STREET:
CITY: BO
STATE: M
COUNTRY:
ZIP: 021
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PCT-US95-13841
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DB 3; LC..50e-08;
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      Score 152; DB 3
Pred. No. 1.50e-
0; Mismatches
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completed: Tue Aug 17 16:11:20 1999
ne : 7 secs.
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Matches 2
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ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 19,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFHONE: (516)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                       Score 152; DB 2;
Pred. No. 1.50e-08
0; Mismatches
                                                           us2
APPLICATION.
FILING DATE: 27-h.
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: linear

TYPE: peptide

TYPE: peptide
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                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 22 AA; 2606 MW;
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Best Local Similarity 100.0%;
Matches 20; Conservative
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Pred. No. 1.50e-08;
0; Mismatches 0;
        3203 CN;
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2606 MW; 3
                         Similarity 100.0%; 20; Conservative
MOLECULE TYPE: SEQUENCE 22 AA;
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.18 Seconds 114.914 Million cell updates/sec Run on:

Tue Aug 17 15:58:29 1999;

not generated. output Tabular

>US-09-049-847-3 (1-12) from US09049847.pep 82 1 GQIGNDPNRDIL 12 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

122810 seqs, 40068593 residues

Searched:

Minimum Match 08 Listing first 45 summaries Post-processing:

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

scale 0.837 Variance 28.469; Mean 23.828; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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The source of this protein was an extrachromosomal plasmid.

The precursor is cleaved by endogenous proteinase activity to form igner (fragment A) and heavy (fragment B.C) chains that are covalently linked by an interchain disulfide bond (the individual chains are not toxic when separated). The amino end of the heavy chain (fragment B) can be separated from the carboxyl end (fragment C) by papain.

Fragment B forms ion channels in a lipid bilayer. Fragment C bind; to gangliosides and may target the toxin to the motor end plate Fragment A is a zinc-dependent endopeptidase.

This potent neurotoxin binds to peripheral neuronal synapses, is internalized, and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and proteolytic cleavage of synaptobrevin (vesicle-associated membrane protein 2).
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Schiavo, G.; Benfenati, F.; Poulain, B.

Laureto, P.P.; DasGupta, B.R.; Montec

Nature (1992) 359:832-835

Tetanus and botulinum-B neurotoxins blorelease by proteolytic cleavage of sy

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                                                                                                                                     Shaw, D.R.; Ennis, H.L.
Biochem. Biophys. Res. Commun. (1993) 193:1291-12
Molecular cloning and developmental regulation of Dictyostelium discoideum homologues of the huma HIV1 Tat-binding protein.
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H.
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Schnall, R.; Mannhaupt, G.; Stucka, R.; Tau
Schwarzlose, C.; Vetter, I.; Feldmann, H
Yeast (1994) 10:1141-1155
Identification of a set of yeast genes codi
family of putative ATPases with high simi
constituents of the 26S protease complex
ices MUID:95274317
                                                                                                                                                                                                                                                   ues 1-403 ##label SHA
-references GB:L16578; NID:g290054; PID:g290055
N #superfamily ATP-dependent 26S proteinase;
FtsH/SEC18/CDC48-type ATP-binding domain ATP; nucleus; P-1000
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protein YDR394w; YTA2 protein
#formal_name Saccharomyces cerevisiae
22-Aug-1996 #sequence_revision 06-Sep-15
13-Sep-1998
S69678; S46606; S34353
S69665
Dietrich, F.S.
Submitted to the EMBL Data Library, July
The sequence of S. cerevisiae cosmids 94
and lambda 3641.
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#length 403 #molecular-weight 4554
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Pred. No. 2.85e+
1; Mismatches
probable transcription factor Dd (Dictyostelium discoideum)

Tat-binding protein 2
#formal_name Dictyostelium discoideum)
31-Dec-1993 #sequence_revision 3.
04-Sep-1998
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s EMBL:X73570;
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-references EMBL:U32274;
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##status nucle
##molecule_type DNA
##residues 1-341
##cross-references EN
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genome polyprotein - yellow fever virus (strain 17D)
capsid protein C; envelope protein M; major envelope prot
E; nonstructural protein NS1; nonstructural protein NS3;
nonstructural protein NS4a; nonstructural protein NS3;
nonstructural protein NS5
#formal_name yellow fever virus
27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change
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A03914
Rice, C.M.; Lenches, E.M.; Eddy, S.R.; Shin, R.L.; Strauss, J.H.
Science (1985) 229:726-733
Nucleotide sequence of yellow fever virus: im
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Pred.
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SGD:RPT3; YTA2; YNI1
##cross-references SGD:S0002802,
#map_position 4R
CLASSIFICATION #summer
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Library, April 1989, in computer-readable for
#superfamily yellow fever virus genome polyprotein;
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nonstructural protein; P-loop; polyprotein; transmensi
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1796,2062,2320,
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2720,2734,2740
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##molecule_type DNA
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##molecule_type I
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GTP cyclohydrolase I (folE) RP383 - Rickettsia prowazekii
#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change
21-Nov-1998
F71695
A71630
Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.;
Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.;
Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland,
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#region nucleotide-binding motif A
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#product nonstructural protein NS48
#label N4A\
#product nonstructural protein NS48
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##molecule_type DNA
##residues 1-190 ##label AND
##cross-references GB:AJ235271; GI
##cross-references GB:AJ235271; GI
##cross-references GB:AJ235271; GI
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Aubusto Kunst, F.; Gassawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Bronillet, S.; Brans, Daniel, C.V.; Caldwell, S.C.; Bron, S.; Bronillet, S.; Brans, Daniel, R.W.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Ehrlich, S.D.; Emmerson, P.; Fritz, C.; Fujita, F.; Fulla, K.D.; Errington, J.; Endret, C.; Furi, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleon, N.; Ghim, S.Y.; Glaser, P.; Goffens, E.J.; Galizzi, A.; Hascon, N.; Galiseppi, G.; Guy, B.J.; Haga, K.; Haisopp, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, W.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, X.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Mosell, D.; Nakai, S.; Noback, M.; Mosel, D.; Nakai, S.; Noback, M.; Ravolta, G.; Brapport, G.; Reche, B.; Rose, M.; Sadaie, Y.; Sarlo, T.; Scallon, E.; Schreiter, R.; Schreiter, R.; Schreiter, R.; Schreiter, R.; Schreiter, R.; Schreiter, R.; Serrer, P.; Schleich, S.; Schroeter, R.; Schreiter, R.; Schreiter, R.; Schreiter, R.; Serrer, R.; Schreiter, R.; Vasacrott, A.; Tarawa, H.; Panchin, A.; Tanakaa, H.; Tanaka, H.; Tanama, H.; Panchin, A.; Tanama, H.; Ta
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^s, P.;
· Brans,
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Molecular cloning, nucleotide sequence, and ch of the Bacillus subtilis gene encoding the D
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##cross-references GB:X52418
NCE A69580
     he mtr locus is a attenuation in ses MUID:91062353
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Shen, S.H.; Chretien, P.; Bastien, L.; Slilaty, J. Biol. Chem. (1991) 266:1058-1063
Primary sequence of the glucanase gene from Oer xanthineolytica. Expression and purification from Escherichia coli.
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Chambers, P.; Millar, N.S.; Platt, S.G.; Em Nucleic Acids Res. (1986) 14:9051-9061
Nucleotide sequence of the gene encoding th of Newcastle disease virus.

references MUID:87066775
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17-Feb-1994 #sequence_revision 17-Feb-1994 #text_
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Jen. Virol. (1992) 73:2785-2793
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GTP cyclohydrolase I (EC 3.5.4.16) - Mycobacterium
tuberculosis (strain H37RV)
#formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
21-Nov-1998
B70956
A70500
Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barz
III, C.E.; Tekaia, F.; Badcock, R.; Basham, D.; Brown, D.;
Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Rutter, S.; Seeger, K.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.;
Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
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##residues 1-202 ##label COL
##cross-references GB:295557; GB:AL123456; NID:93242276;
##cross-references GB:295557; GB:AL123456; NID:93242276;
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#formal_name Saccharomyces cerevisiae
30-Jun-1992 #sequence_revision 30-Jun-
12-Jun-1998
JX0182; PS0224; A39376; S15050; JS0634
S19372; S25349
                           1-decarboxylase
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(Saccharomyces cerevisiae)
otein YCL043c; protein YCL313; S-S
thioredoxin-related glycoprotein 1;
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'S',459-505,'EADAEAEA',506-522 ##label GUI
S GB:M76982; NID:g173023; PID:g173024
                                                                                                                                                                                                                                                             H.; Kaplan,
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LaMantia, M.; Miura, T.; Tachikawa, H.; Kaplan,
Lennarz, W.J.; Mizunaga, T.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4453-44
Glycosylation site binding protein and protein
isomerase are identical and essential for cel
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Freedman, R
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'S',459-505,'EADAEAEA',506-522 ##label
-references EMBL:X52313; NID:g3948; PID:g3949
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J. Biol. Chem. (1991) 266:24557-24563

The Saccharomyces cerevisiae TRG1 gene is est growth and encodes a lumenal endoplasmic registrences MUID:92105117

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 Tachikawa, H.; Miura, T.; Katakura, J. Biochem. (1991) 110:306-313
Molecular structure of a yeast gene disulfide isomerase that is essenuces MUID:92105067
                                                                                                                                                                      #molecule_type protein
#residues 99-112;'X',185-193;211-217;'X'
"x',288-298;309-315;325-335
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, F.; Scherens,
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S15050
Scherens, B.; Dubois, E.
Yeast (1991) 7:185-193
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##molecule_type DNA
##residues 1-113,'R',115-5(
##cross-references EMBL:X54535;
NCE S40913
                                                                                                                 ##cross-references GB:D00842;
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BEM4 protein - yeast (Saccharomyces cere
protein P2561; protein YPL161c
#formal_name Saccharomyces cerevisiae
03-May-1994 #sequence_revision 02-Aug-19
06-Feb-1998
S45177; S65172; S69438
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Mack, D.; Bender, A.
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Scherens, B.; Messenguy, F
Yeast (1992) 8:577-586
The complete sequence of a
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PID:e247048; PID:g1370342;
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#description The sequence of 55 kb on the left arm of yeast chromosome;
identifies 28 open reading frames including 18 unknown among which a new putative serine/threonine protein kinase a homologue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant pleiotropic regulator PRL1 of PP1 and PP2a phosphatases.

##molecule_type DNA ##molecule_type DNA ##label prw
##scoss.references EMBL:X96770; NID:g1403537; PID:e239041; PID:g140354
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Pred. No. 7.43e+00;
1; Mismatches 2;
##cross-references EMBL:Z73517; NID:g1370341;
MIPS:YPL161c
##experimental_source strain S288C (AB972)
REFERENCE S69428
#authors Purnelle, B.; Comblez, S.; Coster,
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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>US-09-049-847-3 (1-12) from US09049847.pep 82 1 GOIGNDDWD--Title: Description: Perfect Score: Sequence:

Scoring table:

77977 seqs, 28268293 residues PAM 150 Gap 15 Searched:

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swiss-prot37
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.953

Variance 25.693;

Mean 24.484;

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BEM4 PROTEIN.	DELTA-(L-ALPHA-AMINOAD	PROTEIN-TYROSINE PHOSP	GTP CYCLOHYDROLASE I (HYPOTHETICAL 29.7 KD P	NADH-PLASTOQUINONE OXI	INE	۳	URACIL-DNA GLYCOSYLASE	ELA P	B PROTEIN (FRAGME	LUCOSE DEHYDROGENAS	N KINASE SPK1 (OTEIN KDPD (HOSPHATIDYLINOSI	\mathcal{O}	8	TRYPTOPHAN SYNTHASE BE	DASE B PR	LIODEXTRIN GL	N FACTOR 2 (INESIN-LIKE PROTE
EM4_	ACVS_EMENI	CSW_DROME	GCH1_CAMJE	YEV6_YEAST	NU4C_TOBAC	PUR2_YEAST	IMB3_HUMAN	UNGI_BPPB2	KLAB_ECOLI	TFEB_HUMAN	DHG_ECOLI	SPK1_YEAST		PI4K_DICDI	MET_MOUSE	MSP1_PLAYO	TRPB_HAEIN	CBPB_HUMAN	CDGT_KLEPN	EF2_BLAHO	BIMC_EMENI
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ALIGNMENTS

RESULT 1 ID TETX_CLOTE STANDARD; PRT; 1314 AA. AC P04958;	13-AUG-1987 (REL. 05, 13-AUG-1987 (REL. 05,	15-JUL-1998 (REL. 36, LAST ANNOTATIO TETANUS TOXIN PRECURSOR (EC 3.4.24.6	CLOSTRIDIUM TETANI.	THE TAXABLE SET THE SET OF SET		CC CLOSIAIDIOM: RN [1]	SEQUENCE	MEDLINE; 870538	EISEL U., JARAUSCH W., GORETZKI K., HENSCHE	WELLER U., HUDEL M., HABERMANN E., NIEMANN H.;	imary structu		[2]				FAIRWEATHER N.F., LYNESS		NUCLEIC ACIDS RES. 14:780	KN [3] RD SECTENCE OF 742-1914 EDOM N N	MEDITAR: 86085670	E., LYNESS V.A., PICKARD D.T. ALLEN	"Cloning, nucleotide sequencing, and expression of tetanns town	fragment C in Escherichia coli.";		מתדם יוויסדת תואג מסי		KRIEGLSTEIN K., HENSCHEN A., WELLER U	"Arrangement of disulfide bridges and positions of sulfhydryl	in tetanus toxin.";		[5]	PARTIAL SEQUEN	MEDLINE; 92037	KRIEGLST	"Limited proteolysis of tetanus toxin. Relation to act		EUR. J. RIOCHEM 202-41-51719917) T
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EMBL: X04436: GA0770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE AND ARE NON-TOXIC AFTER SEPARATION.

THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO GANGLIOSIDE RECEPTORS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76-GLN-|-PHE-7
                                                                                                                                                                                                                                                                     release
                                                                                                                                                                                                                                                                                                                                                                                           S., FUREY W.F., SCHMIDT J.J
                                                                                                                                                                                                                            д.
Р.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUROTRANSMITTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrictive by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC;
                                                                                                                                                                                                                                                                    neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurotoxin.";

NAT. STRUCT. BIOL. 4:788-792(1997).

-!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMI
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS I
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-G
BOND OF SYNAPTOBREVIN-2.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-|-PHE-77 BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                   tetanus
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EMBL; X12739; G144921; -.

EMBL; X06214; G40774; -.

PIR; A25689; BTCLTN.

PDB; 1AF9; 29-APR-98.

PROSITE; PS00142; ZINC_PROTEASE; 1.

NEUROTOXIN; TRANSMEMBRANE; HYDROLASE; METALLOPROTEASE;

3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETANUS TOXIN LIGHT CHAIN.
TETANUS TOXIN HEAVY CHAIN.
ZINC (CATALYTIC) (BY SIMII
BY SIMILARITY.
                                                                                                   of
                                                                                                                      depend
                                                                                                     its inhibition
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                                                                                                                                                                                                                         NFENATI F., POULAIN B., ROSSETTO
MONTECUCCO C.;
otulinum-B neurotoxins block neur
cleavage of synaptobrevin.";
                                                                                                                      and protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment HC
                                                             BENFENATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY.
(C (CATALYTIC)
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MEDLINE; 97475217.
UMLAND T.C., WINGERT L.M., SWAMINATHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 82;
Pred. No.
0; Mism
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r release and prot
-3583(1992).
                                                           ROSSETTO
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                   ZINC-PROTEASE
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"Structure of the receptor neurotoxin.";
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larity 100.0%;
Conservative
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DASGUPTA B.R., MONTECCOL.
"Tetanus and botulinum-B not protective cleavage of by protective cleavage of by protective cleavage of the protection of the protection
                                                         m.,
                                                                                                                                                                                 identification of Subsmediine; 93063293.
                DENTIFICATION AS ZI
EDLINE; 93010948.
CHIAVO G., POULAIN
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AA;
                                  MEDLINE; 93010948.
SCHIAVO G., POULAII
MONTECUCCO C.;
"Tetanus toxin is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNAPTOBREVIN.
                                                                                                                     neurotransmitter
EMBO J. 11:3577-3
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SEQUENCE
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Best Local
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nd for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                     e EMBL outstation restrictions on i
                                                                                                                                                                                                                                             FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE) COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE 26S COMPLEX (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).

DEVELOPMENTAL STAGE: HIGHEST EXPRESSION IN VEGETATIVELY GROWING CELLS. THE LEVEL OF EXPRESSION FALLS STEADILY THROUGHOUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRS6_SOLTU STANDARD; PRT; 413 AA.

P54778;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG.
SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EURHYLLOPHYTES; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gap
                                                                                                                                                                                                          of Dictyostelium
                                                                            PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a clearmen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                         (TAT-BINDING
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                                                                                                                                                                                                           regulation
nd yeast HIV
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. No. 9.41e-01;
Mismatches 3
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F1A7C9A7 CRC32
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FJ
                                    28, CREATED)
28, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE
ATORY SUBUNIT 6B HOMOLOG (
                                                                                                                                                                                                                                                                                                                                                                                   THE AAA FAMILY
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PROTEASOME; ATP-BINDING; NUCLEAR PROTEIN
                                                                                                                 (SLIME MOLD).
           03
                                                                                                                                                                                                                       human and
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Pred. No.
1; Misma
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:y 63.6%;
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DICTYOSTELIUM DISCOIDEUM (
EUKARYOTA; DICTYOSTELIIDA;
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DICTYDB; DD01052; TBPB.
PROSITE; PS00674; AAA; 1.
                                                                                                                                                                                                                         of
                                    (REL. 28, CR
(REL. 28, LA
(REL. 36, LA
E REGULATORY
                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=AX4;
MEDLINE; 93312322.
SHAW D.R., ENNIS H.L.;
"Molecular cloning and discoideum homologues of
                                                                                                                                                                                                                                                                                                                                                                    GERMINATING SPORES. SIMILARITY: BELONGS
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G290055;
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QIGNDPNRDIL
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JN0611; J
           PRS6_DICDI
P34123;
01-FEB-1994 (F
01-FEB-1994 (F
15-JUL-1998 (F
26S PROTEASE F
HOMOLOG 2).
                                                                                         2).
TBP2
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SOLTU
2
DICDI
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BIOCHEM. B
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SEQUENCE
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Matches
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                                                                                                      ATPASE)
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-! FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
26S COMPLEX (BY SIMILARITY).

-! SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).

-! SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                    TO THE
          F23F12.6.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROIEASOME; ATP-BINDING; NUCLEAR PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 413
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. No. 9.41e-01;
Mismatches 3
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL).
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LAST ANNOTATION UPDATE)
REGULATORY SUBUNIT 6B.
                                                                                                                                                                                                                                                                                                                    04; AAA; 1.
ATP-BINDING; NUCLEAR PROTEIN.
201 208
                                                                                                                                                                                                                                                                                                                                                                                                   Score 52;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                           ATP
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larity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U12965; G529215; -. WORMPEP; F23F12.6; CE01253. PROSITE; PS00674; AAA; 1.
                                                                                                                                                                                                                                                                                                U43398; G1155334; -
IE; PS00674; AAA; 1.
PF00004; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, C
01-NOV-1995 (REL. 32, L
15-JUL-1998 (REL. 36, L
PROBABLE 26S PROTEASE R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00004; AAA; 1 IETICAL PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                                                                      413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIGNDPNRDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIGIDPPRGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N. STRAIN-BRISTOL N. DU Z.;
                                                                                                                                                                                                                                                                                                                                                                                                               Simila:
7; Cc
SEQUENCE FROSTRAIN=CV. SHART J.K., I Isolation (IN) PLANT (IN) -1- FUNCTION
                                                                                                                                                                                                                                                                                                                                          PROTEASOME;
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRS6_CAEEL
P46502;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Sest Local S
                                                                                                                                                                                                                                                                                                EMBL; U4
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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HYPOTHET
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           R ATPASE)
TO THE
                                                                     Gaps
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highly
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
MEDLINE; 96183075.
MAKINO Y., YOGOSAWA S., KANEMAKI M., YOSHIDA T., YAMANO K.,
KISHIMOTO T., MONCOLLIN V., EGLY J.M., MURAMATSU M., TAMURA T.;
"Structures of the rat proteasomal ATPases: determination of higher structural motifs and rules for their spacing.";
"Structures of the rat proteasomal ATPases: determination of higher structural motifs and rules for their spacing.";
BIOCHEM. BIOPHYS. RES. COMMUN. 220:1049-1054(1996).
-!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ACCOMPLEX CONFERS ATP DEPENDENCY AND SUBSIRATE SPECIFICITY TO
                                                                                                                                                                                                                                                                                 EUTHERIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \circ
                                                                                                                                                                                               (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7)
                                          414
                                                                    Indels
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                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26S COMPLEX.
SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.
SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES
SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                 MAMMALIA;
RATTUS.
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PRS6_MOUSE STANDARD; PRT; 418 AA.
P54775;
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
26S PROTEASE REGULATORY SUBUNIT 6B (CIP21).
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E1F26490 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; FOUND, AAA; 1.
PFAM; PF00004; AAA; 1.
PROTEASOME; ATP-BINDING; NUCLEAR PROTEIN.
NP BIND 206 213 ATP (POTENTIAL)
                                        DB 1;
9.41e
                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 52; DB l;
No. 9.41e-
Mismatches
                                                                                                                                                                                                                                                                             : METAZOA; CHÓRDATA; VERTEBRATA;
SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                         418
                                                                   Misma
                                       Score 52;
Pred. No.
1; Misma
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Pred.
1; M
    ATP
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EUKARYOTA; METAZOA; CHORDATA;
                                      63.48;
larity 63.68;
Conservative
209
46358
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63.68;
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RATTUS NORVEGICUS
EUKARYOTA; METAZOA,
RODENTIA; SCIUROGNA
               AA;
                                                   Similarity 7; Conse
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QIGNDPNRDIL
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01-NOV-1997
15-JUL-1998
26S PROTEASE
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                                     Query Match
Best Local S
Matches
NP_BIND
SEQUENCE
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PRS6_RAT
Q63570;
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ASPERGILLUS
EUKARYOTA; F
EUROTIALES;
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PROTEASOME;
                                                  / Match
Local 9
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Matches
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commenenties requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
                                UE=LIVEK;
H.S., SEOL W., MOORE D.D.;
ITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
                                                                                                                                                                                                                                                                                                                                Gaps
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METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
family c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GREEN M.R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN-7
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                           OF ATPASES.
                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                CYTOPLASMIC AND NUCLEAR
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                                                                                                                                                                                                                                                                                                           -;
e-01;
3;
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(TAT-BINDING
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                                                                                                                                                                                                                                                                           P (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, REVISION TO C-TERMINAL, AND MEDLINE; 94338582.

DÜBIEL W., FERRELL K., RECHSTEINER M.;

"Tat-binding protein 7 is a subunit of the 26 BIOL. CHEM. HOPPE-SEYLER 375:237-240(1994).

-!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN DEGRADATION OF UBIQUITINATED PROTEINS. THE COMPLEX CONFERS ATP DEPENDENCY AND SUBSTI
                                                                                                                                                                                                                                                                                                           e 52; DB 1;
No. 9.41e-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOORE P.A., RUBEN S.M., SOUTHGATE
                                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
S REGULATORY SUBUNIT 6B (TAT-BIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus T
f to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC AND
BLOCKED.
THE AAA FAMILY
                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC AND SIMILARITY: BELONGS TO THE AAA FAMILY
 MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                   418
                                                                                                                                                                                                                               ; L76223; G1196528; -.
;ITE; PS00674; AAA; 1.
[; PF00004; AAA; 1.
;EASOME; ATP-BINDING; NUCLEAR PROTEIN
                                                                                                                                                                                                                                                                                                          Score 52;
Pred. No.
1; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OHANA B., MOORE P.A., RUBEN S.M., SUROSEN C.A.;
"The type 1 human immunodeficiency vtranscriptional activator belonging transcriptional activator belonging
                                                                                                                                                                                                                                                                              ATP
MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed genes.
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PTM: THE N-TERMINAL IS
SIMILARITY: BELONGS TO
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larity 63.6%;
Conservative
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47281
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SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07; -.
PS00674; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMAN)
                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 93126329.
                                                                                                                                                                                                                                                                                        AA;
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                     N.A
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QIGNDPNRDIL
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418 #
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01-NOV-1995 (R)
01-NOV-1995 (R)
15-JUL-1998 (R)
26S PROTEASE R
PSMC4 OR TBP7.
                    SEQUENCE FROM P
TISSUE=LIVER;
CHOI H.S., SEOI
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-!- PTM: THE
-!- SIMILARI
MIM; 602707;
PROSITE; PS0
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PRIMATES; C
                                                                                                                                                                                                                                                                                                                                                                                                                   PRS6_HUMAN
                                                     SUBMITTED
RODENTIA;
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Best Local
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PFAM;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CBS 120.49 / N400;
DELEU C., JARAI G., BUXTON F.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-! FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE 26S COMPLEX (BY SIMILARITY).
-! SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).
-! SUBCELLULAR INCATION: THE AAA FAMILY OF ATPASES.
-! SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-! FMFL OUTSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIGER.
FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Q
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                                                                                                                                                 Indel
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P33298;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG (YNT1 HOMOLOG 2).
YTA2 OR YNT1 OR YDR394W OR D9509.14.
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P (POTENTIAL).
14E49380 CRC32;
                                                                                                                         0.1
                                                                                                                                                                                                                                                                                                                                                          (REL. 36, CREATED)
(REL. 36, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
REGULATORY SUBUNIT 6B HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e 52; DB 1;
. No. 9.41e-C
Mismatches
                    AR PROTEIN.
TP (POTENTIAL).
4D06C2AF CRC32
                                                                                                     e 52; DB 1;
No. 9.41e-
Mismatches
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Pred. No.
1; Misma
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Pred.
1; M
                      NUCLEAR
ATP
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PFAM; PF00004; AAA; 1.
PROTEASOME; ATP-BINDING; NUCLINP_BIND 206 213 SEQUENCE 418 AA; 47336 MW;
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larity 63.6%;
Conservative
                                                                                                    Similarity 63.4%;
7; Conservative
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PROSITE; PS00674; AAA; 1.
PFAM; PF000004; AAA; 1.
                                                                                                                                                                                                                                                                                                                     STANDARD;
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7; Conser
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QIGNDPNRDIL
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QIGNDPNRDIL
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P78578;
15-JUL-1998 (1
15-JUL-1998 (1
15-JUL-1998 (1
26S PROTEASE 1
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                                                                                                                                                                                                             NOSEDALE D., NAKAHARA K., ALLEN E., ARAUJO R., AVILES E.,
A DIETRICH F.S., MULLIGAN J., ALLEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
A BERNO A., CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
A HUNICKE-SMITH S., HYMAN R., KOMP C., LASHKARI D., LEW H., LIN D.,
A MOSEDALE D., NAKAHARA K., NAMATH A., OEFNER P., OH C., PETEL F.X.,
A ROBERTS D., SCHRAMM S., SCHROEDER M., SHOGREN T., SHROFF N.,
A WINANT A., YELION M., BOTSTEIN D., DAVIS R.W.,
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
C.!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
26S COMPLEX (BY SIMILARITY).
COMPLEX (BY SIMILARITY).
C.!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).
C.!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
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C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAB AND SUBSTRATE SAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAA FAMILY OF ATPASES.
C.!- SIMILARITY: BELONGS TO THE BAB AND SUBSTRATE SAMILY OF EMBL OUTSTATE
C.!- SIMILARITY: SELONGS TO THE BAB AND SUBSTRATE SAMILY OF SUBSTRATE SAMILY OF S
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POLG_YEFV1 STANDARD; PRT; 3411 AA.

POLG_YEFV1 STANDARD;

21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)].

YELLOW FEVER VIRUS (STRAIN 17D).

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE; FLAVIVIRUS.
                                                                                            of
                                                                                           el family
the 26S
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BANKS.
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TO EMBL/GENBANK/DDBJ DATA I
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213 220 ATP (POTENTIAL).
342 342 Y -> S (IN REF.
428 AA; 47969 MW; E96A890E CRC32
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. No. 9.41e-
Mismatches
                                                           TAUER
                    STRAIN=C836;
MEDLINE; 95274317.
SCHNALL R., MANNHAUPT G., STUCKA R., TAUER SCHWARZLOSE C., VETTER I., FELDMANN H.; "Identification of a set of yeast genes coputative ATPases with high similarity to c protease complex."; YEAST 10:1141-1155(1994).
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Pred. No.
1; Misma
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EMBL; U06229; G458389; -.
EMBL; U32274; G927327; -.
PIR; S45606; S46606.
SGD; L0002556; YTA2.
PROSITE; PS00674; AAA; 1.
PROTEASOME; ATP-BINDING; N
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larity 63.5%;
Conservative
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SUBMITTED (FEB-1994)
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CONFLICT
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SEQUENCE FROM N.A.

MEDLINE; 85272570.

RICE C.M., LENCHES E.M., EDDY S.R., SHIN S.J., SHEETS R.L.,

STRAUSS J.H.;

"Nucleotide sequence of yellow fever virus: implications for flavivirus gene expression and evolution.";

SCIENCE 229:726-733(1985).

-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS:

PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFERASE; RNA-DIRECTED RNA POLYMERASE;
ENVELOPE PROTEIN; HELICASE; ATP-BINDING;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NONSTRUCTURAL PROTEIN NS2B.
NONSTRUCTURAL PROTEIN NS4B.
HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4B.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (POTENTIAL.
POTENTIAL.
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BY SIMILARITY.
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MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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CELLULAR AMINOPEPTIDASE
CAPSID PROTEIN C,
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POTENTIAL.
MW; E85D316D CRC32;
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EMBL; X02749; G336193; -.
PIR; A03914; GNWVY.

PFAM; PF00869; Flavi_NS1; 1.

PFAM; PF00949; Flavi_NS1; 1.

PFAM; PF01002; Flavi_NS5; 1.

PFAM; PF01003; Flavi_NS5; 1.

PFAM; PF01004; Flavi_NS2B; 1.

PFAM; PF01004; Flavi_M; 1.

PFAM; PF01005; Flavi_M; 1.

PFAM; PF01005; Flavi_M; 1.

PFAM; PF01005; Flavi_M; 1.
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V; COAT PROTEIN; EN
VE; NONSTRUCTURAL E
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D POLG_YEFV2 STANDARD; PRT; 3411 AA.

C P19901;

T 01-FEB-1991 (REL. 17, CREATED)

T 01-FEB-1991 (REL. 37, LAST SEQUENCE UPDATE)

T 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX

E PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL

E PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED

E RNA POLYMERASE (EC 2,7.7.48) (NS5)].

S YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204).

C FLAVIVIRUS.
                             0
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE; 89282413.

MEDLINE; 89282413.

DUPUY A., DESPRES P., CAHOUR A., GIRARD M., BOULOY M.;

"Nucleotide sequence comparison of the genome of two 17D-204 yellow

T ever vaccines.";

NUCLEIC ACIDS RES. 17:3989-3989(1989).

LIPORCHION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE

HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL COVERED BY A LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS:

LIPOPROTEIN AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstat. the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commenenties requires a license agreement (See http://www.isb-sib.ch/annoror send an email to license@isb-sib.ch).
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; ENVELOPE PROTEIN; HELICASE; ATP-BINDING
AL PROTEIN.
REMOVED FROM CAPSID PROTEIN C BY THE
CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C.
                              Gaps
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«o 17D-204 yellow
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MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (
                                N)
                              Indel
  Length
52; DB 1; Len No. 9.41e-01; ismatches 1;
Score 52;
Pred. No.
2; Misma
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PIR; S07757; GNWVYP.

PFAM; PF00869; Flavi_Glycoprot; 1.

PFAM; PF00948; Flavi_NS1; 1.

PFAM; PF00949; Flavi_NS1; 1.

PFAM; PF01002; Flavi_NS2; 1.

PFAM; PF01003; Flavi_NS2B; 1.

PFAM; PF01004; Flavi_NS2B; 1.

PFAM; PF01005; Flavi_NS2B; 1.

PFAM; PF01005; Flavi_NS2B; 1.

PFAM; PF01005; Flavi_NS2A; 1.

RSSP; P14336; 1SVB.

POLYPROTEIN; GLYCOPROTEIN; TRANSFERA; CORE PROTEIN; COAT PROTEIN; ENVELOPE TRANSMEMBRANE; NONSTRUCTURAL PROTEIN
Similarity 70.0% 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
2210
285
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GQIGNDPNRD
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INIT_MET
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J. BACIELL.

[3]

FUNCTION.

MEDLINE; 92202128.

A BABITZKE P., GOLLNICK P., YANOFSKY C.;

The mtrab operon of Bacillus subtilis encodes GTP cyclohydrolase I

(Mtra), an enzyme involved in folic acid biosynthesis, and MtrB, a

regulator of tryptophan biosynthesis.";

J. BACTERIOL. 174:2059-2064(1992).
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transcription
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[4]
CHARACTERIZATION.
MEDLINE; 95194311.
DE SAIZIEU A., VANKAN P., VAN LOON A.P.;
"Enzymic characterization of Bacillus subtilis GTP cyclohydro."
Enzymic characterization of Bacillus subtilis GTP cyclohydro. Evidence for a chemical dephosphorylation of dihydroneopterin triphosphate.";
BIOCHEM. J. 306:371-377(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-19 FROM N.A.

STRAIN=168 / JH642;

MEDLINE; 91216992.

MICKA B., GROCH N., HEINEMANN U., MARAHIEL M.A.;

Molecular cloning, nucleotide sequence, and characterization

Bacillus subtilis gene encoding the DNA-binding protein HBsu.'

J. BACTERIOL. 173:3191-3198(1991).
                                                                                                                                                                                                                                                                                                                                                                          BACILLACEAE
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[1]
SEQUENCE FROM N.A.
MEDLINE; 91062353.
GOLLNICK P., ISHINO S., KURODA M.I., HENNER D.J., Y
The mtr locus is a two-gene operon required for tr
attenuation in the trp operon of Bacillus subtilis.
PROC. NATL. ACAD. SCI. U.S.A. 87:8726-8730(1990).
                                                                                                                                                                                                                                                                                                                                                                 BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                    e-01;
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ADCCF22B CRC32
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P19465;
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GTP CYCLOHYDROLASE I
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no woodified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: GTP + 2 H(2)O = FORMATE + 2-AMINO-4-HYDROXY-6-(ERYTHRO-1,2,3-TRIHYDROXYPROPYL)DIHYDROPTERIDINE TRIPHOSPHATE.
ENZYME REGULATION: K+ IONS MODERATELY INCREASES THE VMAX., WHEREA: UTP AND CA2+ AND MG2+ IONS DRASTICALLY INCREASE THES KM FOR GTP.
PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF TETRAHYDROFOLATE.
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NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/45) (NDV).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; RUBULAVIRUS.
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MEDLINE; 87066775.
CHAMBERS P., MILLAR N.S., PLATT S.G., EMME "Nucleotide sequence of the gene encoding Newcastle disease virus.";
NUCLEIC ACIDS RES. 14:9051-9061(1986).
-! FUNCTION: THE M PROTEIN HAS A CRUCIAL AND INTERACTS WITH THE RNP COMPLEX AS
                                                                                                                                                                        Score Pred. 12; M.
                    - ENZYME REGULATION: K+ IONS M
UTP AND CA2+ AND MG2+ IONS D
PATHWAY: FIRST STEP IN THE B
SUBUNIT: HOMOPOLYMER.
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larity 70.0%;
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SEQUENCE 364 A
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P06157;
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P46507;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
26S PROTEASE REGULATORY SUBUNIT 6B (ATPASE MS73).
MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; LEPIDOPTERA; SPHINGIODEA; SPHINGIDAE; SPHINGINAE;
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TISSUE=INTERSEGMENTAL MUSCLE;
MEDLINE; 95130567.
DAWSON S.P., ARNOLD J., MAYER N.J., REYNOLDS S., BILLETT M.;
GORDON C., COLLEAUX L., KLOETZEL P., TANAKA K., MAYER R.J.;
"Developmental changes of the 26 S proteasome in abdominal intersegmental muscles of Manduca sexta during programmed cannot be seen that the contraction of the cannot be seen that muscles of manduca sexta during programmed cannot be seen that the ca
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ARABINOGALACIAN ENDO-1,4-BETA
GALACTOSIDASE.
5604C50F CRC32;
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3; Mismatches
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE
ARABINOGALACTAN ENDO-1,4-BETA-GALACTOSIDASE
(ENDO-1,4-BETA-GALACTANASE) (GALACTANASE).
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STRAIN=SP. CELLULOSA;
BRAITHWAITE K.L., GILBERT H.J.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF
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SIMILARITY: BELONGS TO FAMILY
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BACTERIA; GAMMA
PSEUDOMONAS.
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R. J. BIOL. CHEM. 270:1850-1858(1995).

C. I. FUNCTION: THE 26 PROTEASE IS INVOLVED IN THE ATP-DEPENDENT

DEGRADATION OF UBICUITINATED PROTEINS. THE REGULATORY (OR ATPASE)

C. OCHALEX.

C. OCHALEX.

C. SUBCELLULAR LOCALION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).

C. IN THE PRE-ECLOSION PERIOD.

C. IN THE P
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Search completed: Tue Aug 17 15:59:18 1999 Job time : 7 secs.

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protein database search, using Smith-Waterman algorithm protein MPsrch_pp

MasPar time 5.83 Seconds 112.413 Million cell updates/sec

Tue Aug 17 15:59:34 1999; Run on:

>US-09-049-847-3 (1-12) from US09049847.pep 82 Title: Description: Perfect Score

not generated.

output

Tabular

GOIGNDPNRDIL Sequence

PAM 150 Gap 15

table:

Scoring

residues 179066 segs, 54579741 Searched

summaries

0 8 4 5 Minimum Match Listing first Post-processing

Database

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Variance 25.076; Mean 23.731;

Statistics

scale 0.946

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	9 KD P 1 368-0	286+0	1.28e+	.28e+0	URSOR. 1.28e+0	URSOR. 1.28e+0	1.28e+0	. 28e+	200+0). 2.20e+0	2.20e+	.20e+0	.20e+0	.20e+0	ς.	(FRAG 2.20e+0	.76e+0	.76e+0	SE I. 6.38e+	SE I. 6.38e+0
Description	YPOTHETICAL 51	S PROTEASE RE	OLYPROTEIN,		PR			OLYPROTEI	REPILIN.	CLIN	YCLIN K.	TRI	MATRIX PROTEIN.	MATRIX PROTEIN.	MATRIX PROTEIN.	KIAA0589 PROTEIN		5263.	CLOHYD	TP CYCLOHYDRO
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Sco:	56	52	52	52	52	52	52	52	51	51	51	51	51	51	51	51	50	50	49	49
sult No.	1 1 1 1 1 1	2	ന	7	വ	9		∞	თ			12								

386+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.07e+0	.07e+0	.07e+0	.07e+0	.07e+0	.79e+0	.79e+0	.79e+0	.79e+0	.79e+0	.79e+0	.79e+0	.79e+0	.79e+0	
POTHETICAL 44.2 KD	CTINESTERASE (EC 3	CTINESTERASE (EC 3.	TATIVE GDH.	RKSCREW PROTEIN (E)	RKSCREW PROTEIN Y12	RKSCREW PROTEIN 4A	SMEMBRANE PROTEIN	ECKS.	2G12.5 PRO	THYLMALONYL-COA MUT	P CYCLOHYDROLASE	LYMERASE-ASSOCIATED	UTAMINE-BINDING P	GULATORY PROTEIN VI	F GENE (STRAIN KU8)	OBABLE DNA-BINDING	POTHETICAL 31.6 K	OG12.1 PROTEI	TRIX PROTEI	HETICAL 58.8 KD	HOSPHATIDYLINOSITOL-	ASE (EC 1.11.1.	AN-GTP BINDING PROTE	OTCH HOMCLOG.
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							28																	

ALIGNMENTS

ESULT 1 D 051898	[1] SEQUENCE STRAIN=R- MEDLINE; CASJENS SHUANG W.N "Telomere nucleotic telomeres MOL. MICH EMBL; AFC HYPOTHETI	Query Match Suest Docal Similarity 54.5%; Score 56; DB 2; Length 473; Best Local Similarity 54.5%; Pred. No. 1.36e-01; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps Db 36 QIGDGPKREII 46	RESULT 2 CO74894 PRELIMINARY; PRT; 389 AA. CO74894; CO74894; D1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) STORY O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) SCALZOSACCHAROMYCES POMBE (FISSION YEAST). SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE; SCHIZOSACCHAROMYCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simila
7;
                                                                                                               YELLOW FEVER
VIRUSES; SSRN
FLAVIVIRUS.
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Q89275
Q89275;
01-NOV-1996
01-NOV-1996
01-NOV-1998
POLYPROTEIN 1
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    LT 4

Q89277

Q89277;

01-NOV-1996

01-NOV-1996

01-NOV-1998

POLYPROTEIN.
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                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
SEQUENCE FROM N.A.
STRAIN=972H-;
WOOD V., RAJANDREAM M.A., BARRELL B.G., MURPHY L.
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BA
EMBL; AL031798; E1326286; -.
PROSITE; PS00674; AAA; 1.
PROTEASE.
SEQUENCE 389 AA; 43553 MW; E4007B60 CRC32;
SEQUENCE 389 AA; 43553 MW; E4007B63; Ler
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                                                                                                                                              e 52; DB 3; Le
. No. 1.28e+00;
Mismatches 3;
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ENVELOPE PROTEIN ENSI.
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NS2B.
NS3.
NS4A.
NS4B.
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Q89278

Q89278;

O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE O1-NOV-1998 (TREMBLREL. O8, LAST ANNOTATIO POLYPROTEIN.
YELLOW FEVER VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NOFLAVIVIRUS.

[11]
SEQUENCE FROM N.A.
STRAIN=FRENCH VISCEROTROPIC VIRUS;
MEDLINE; 96068808.
WANG E., RYMAN K.D., JENNINGS A.D., WOOD D SANDERS P.G., BARRETT A.D.;
"Comparison of the genomes of the wild-typ strain of yellow fever virus with its vaccineurotropic vaccine.";
J. GEN. VIROL. 76:2749-2755(1995).
                                                                                                                                                                                                                                                                                                          3410
                                                                                                                                                Score 52;
Pred. No.
1; Misma
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Pred.
2; M
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VISCEROTROPIC VIRUS
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SUBMITTED (FEB-1995) TO EMBL/GENB
EMBL; U21056; G694116; -.
PFAM; PF00869; Flavi_NSl; 1.
PFAM; PF00948; Flavi_NSl; 1.
PFAM; PF00972; Flavi_Nelicase; 1.
PFAM; PF01002; Flavi_NS5; 1.
PFAM; PF01003; Flavi_Capsid; 1.
PFAM; PF01004; Flavi_NS2B; 1.
PFAM; PF01005; Flavi_NS2B; 1.
PFAM; PF01005; Flavi_NS2B; 1.
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777
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1482
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2393
2505
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Similarity 63.6%;
7; Conservative
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QIGNDPNRDIL
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11354
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23064
23064
3410
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SEQUENCE FROM 1
STRAIN=FRENCH 7
WANG E.;
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П.
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LAST ANNOTATION UPDATE)
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Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                              M PROTEIN.
ENVELOPE PROTEIN
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SSRNA POSITIVE-STRAND VIRUSES,
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                                                                                                                                                         A.D.,
                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FRENCH NEUROTROPIC VIRUS;
MEDLINE; 96068808.
WANG E., RYMAN K.D., JENNINGS A.D.,
SANDERS P.G., BARRETT A.D.;
"Comparison of the genomes of the w
strain of yellow fever virus with i
neurotropic vaccine.";
J. GEN. VIROL. 76:2749-2755(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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NS2A.
NS2B.
NS3.
NS4A.
NS4B.
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Pred.
2; M
                                                                                                                                                                                                                                                                       SUBMITTED (FEB-1995) TO EMBL/GENB

EMBL; U21055; G1314242; -.

PFAM; PF00869; Flavi_glycoprot; 1

PFAM; PF00949; Flavi_helicase; 1.

PFAM; PF00972; Flavi_helicase; 1.

PFAM; PF01002; Flavi_NS5; 1.

PFAM; PF01003; Flavi_Capsid; 1.

PFAM; PF01004; Flavi_M; 1.

PFAM; PF01005; Flavi_M; 1.
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FLAVIVIRUS.
[1]
SEQUENCE FROM N.A.
STRAIN=VACCINE STRAIN 17DD;
DOS SANTOS C.N., POST P.R., CARV, GALLER R.;
VIRUS RES. 35:35-41(1994).
[2]
                                                                                                                                                                                                                                                       VIRUS;
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larity 70.0%;
Conservative
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NEUROTROPIC
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PRELIMINARY;
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(TREMBLREL.
(TREMBLREL.
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(TREMBLREL.
(TREMBLREL.
PRECURSOR.
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No. 1.28e
Mismatches
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Pred. No. 3; Misma
                         Score 52;
Pred. No.
2; Misma
   NS5
MW;
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                         63.4%;
larity 70.0%;
Conservative
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          AA;
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  2506
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GQIGNDPNRD
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                             re 52; DB 14; L
d. No. 1.28e+00;
Mismatches 1;
                                                                                                                                                                                 CRC32;
                         DATA
                                                                                                                                                                                                                                                                                                                                  NO DNA
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                                                                                                                                                                                                                                                             SULT 6
Q89276
Q89276
Q89276;
Q89276;
O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE O1-NOV-1998 (TREMBLREL. O8, LAST ANNOTATIO POLYPROTEIN PRECURSOR.
YELLOW FEVER VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NC FLAVIVIRUS.

[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=VACCINE STRAIN 17D-213;
DOS SANTOS C.N., POST P.R., CARVALHO R., I
                        TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                06C3D225
                                                                                                                                POTENTIAL.
POTENTIAL.
NS3.
POTENTIAL.
POTENTIAL.
                                                                                                           M PROTEIN.
ENVELOPE P
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ENVELOPE P
NSI.
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PUTATIVE
PUTATIVE
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PUTATIVE
PUTATIVE
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                                                                                                                                                                       NS5.
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VIRUS RES. 35:35-41(1994).
[2]
SEQUENCE FROM N.A.
STRAIN=VACCINE STRAIN 17D-213;
GALLER R.;
SUBMITTED (NOV-1994) TO EMBL/GENBENBL; U17067; G829369; -.
PFAM; PF00948; Flavi_NS1; 1.
PFAM; PF00949; Flavi_NS1; 1.
PFAM; PF01002; Flavi_NS5; 1.
PFAM; PF01002; Flavi_Capsid; 1.
PFAM; PF01003; Flavi_Capsid; 1.
PFAM; PF01005; Flavi_NS2B; 1.
PFAM; PF01005; Flavi_NS2B; 1.
PFAM; PF01005; Flavi_NS2B; 1.
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                     SUBMITTED (NOV-1994) TO EMBL/GENB

EMBL; U17066; G829367; -.

PFAM; PF00869; Flavi_glycoprot; 1

PFAM; PF00948; Flavi_NS1; 1.

PFAM; PF00949; Flavi_NS5; 1.

PFAM; PF01002; Flavi_NS2B; 1.

PFAM; PF01003; Flavi_Capsid; 1.

PFAM; PF01004; Flavi_M; 1.

PFAM; PF01005; Flavi_M; 1.

PCLYPROTEIN.

CHAIN

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GQIGNDPNRD
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285
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778
1187
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SEQUENCE FROM N
STRAIN=VACCINE (GALLER R.;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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091857
091857
091857;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN.
YELLOW FEVER VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STRFLAVIVIRUS.
[1]
SEQUENCE FROM N.A.
STRAIN=17D-204-USA VACCINE;
MEDLINE; 98376360.
XIE H., CASS A.R., BARRETT A.D.T.;
"Yellow fever 17D vaccine virus isolated from head accumulates very few mutations.";
VIRUS RES. 55:93-99(1998).
EMBL; AF052438; G3288892; -.
POLYPROTEIN.
SEQUENCE 3411 AA; 379584 MW; 1C9F6704 CRC32;
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. No. 1.28e+00;
Mismatches 1;
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D225424D CRC32
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Cdk-activating
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VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALE:
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; RUBULAVIRUS.
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kinase and CdJ
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                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
CATARRHINI; HOMINIDAE; HOMO.
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LAST SEQUENCE UPDATE)
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            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
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ANNOTATION UPDATE
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|. No. 2.20e+00;
| Mismatches 2;
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. No. 2.20e+00;
Mismatches 1;
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SEQUENCE FROM N.A.
STRAIN=F48E9;
CHEN H., LIU S., CHEN J., ZHANG B., LU J.;
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF089819; G3695291; -.
MATRIX PROTEIN.
SEQUENCE 364 AA; 39783 MW; B7CE8893 CRC32;
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                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 98298273.
EDWARDS M.C., WONG C., ELLEDGE S.J.;
"Human cyclin K, a novel RNA polymerase II possessing both carboxy-terminal domain ki kinase activity.";
MOL. CELL. BIOL. 18:4291-4300(1998).
EMBL; AF060515; G3746549; -.
SEQUENCE 357 AA; 41293 MW; 547C5CE6 CF
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Pred. No. 5; Mismal
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LAST SEQI
LAST ANNO
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O83834;

O83834;

O1-83834;

O1-NOV-1996 (TREMBLREL. O1, CREATED)

O1-NOV-1998 (TREMBLREL. O8, LAST SEC

O1-NOV-1998 (TREMBLREL. O8, LAST AND MATRIX PROTEIN.

NEWCASTLE DISEASE VIRUS (NDV).

VIRUSES; SSRNA NEGATIVE-STRAND VIRUS

PARAMYXOVIRIDAE; PARAMYXOVIRINAE; RI
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                                                                                                                                                                                                                                                       Score
Pred.
6; M
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08,
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Local Similarity 41.7%;
les 5; Conservative
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Best Local Similarity 41.7%;
Matches 5; Conservative
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092330
092330;
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
MATRIX PROTEIN.
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GQIGNDPNRDIL
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SEQUENCE FROM N
STRAIN=KIMBER;
SEAL B.S.;
VIRUS GENES 11:
O75909;
01-NOV-1998
01-NOV-1998
01-NOV-1998
CYCLIN K.
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serologically defined
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inase and Cdk-activating
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;; MUS.
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LAST ANNOTATION UPDATE)
                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Mismatches 1;
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MEDLINE; 98298273.
EDWARDS M.C., WONG C., ELLEDGE S.J.;
"Human cyclin K, a novel RNA polymerase II possessing both carboxy-terminal domain ki kinase activity.";
MOL. CELL. BIOL. 18:4291-4300(1998).
EMBL; AF060517; G3746552; -.
NON_TER 206 206
CFCTENCE 206 AA; 24071 MW; A154D984 C)
                                                                SULT 9
Q59508
Q59508,
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIC PREPILIN.
MORAXELLA BOVIS.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISIC MORAXELLACEAE; MORAXELLA.
[1]
SEQUENCE FROM N.A.
SIRAIN=3W07 / SEROGROUP B;
MEDLINE; 94327452.
ATWELL J.L., TENNENI J.M., LEPPER A.W., EI "Characterization of pilin genes from seve prototype strains of Moraxella bovis."; J. BACTERIOL. 176:4875-4882(1994).
EMBL; L32969; G488318; -.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
PFRAM; PF00114; pilin; 1.
METHYLATION.
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088874
088874;
088874;
01-NOV-1998 (TREMBLREL. 08, LAST 8
CYCLIN K (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VER'
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Pred.
2; N
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Local Similarity 41.7%;
les 5; Conservative
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larity 66.7%;
Conservative
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| || :|:|||
GQIGNDPNRDIL 12
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GQIGNDPNRDIL
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GQIGNDPNRD
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Local

Query Best L

Matches

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Gaps

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RESULT 11 ID 075909

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Matches

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O83838

O83838

O83838

O83838

O1-NOV-1996 (TREMBLREL. 01, CREATED)

O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

MATRIX PROTEIN.

NEWCASTLE DISEASE VIRUS (NDV).

VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;

PARAMYXOVIRIDAE; PARAMYXOVIRINAE; RUBULAVIRUS.

SEQUENCE FROM N.A.

SEAL B.S.;

L VIRUS GENES 11:217-224(1996).

E WBL; U25835; G1016667; -.

E WBL; U25835; G1016667; -.

E WBL; NATRIX PROTEIN.

SEQUENCE 364 AA; 39464 MW; 72A78A51 CRC32;
                                                                                                                      364;
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                                                                                                                                                                  Indels
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Q83840;
Q83840;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MATRIX PROTEIN.
NEWCASTLE DISEASE VIRUS (NDV).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
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. No. 2.20e+00;
... Mismatches 2;
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. No. 2.20e+00;
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SEQUENCE FROM N.A.
STRAIN=ULSTER;
SEAL B.S.;
VIRUS GENES 11:217-224(1996).
EMBL; U25837; G1016671; -.
PFAM; PF00661; Matrix; 1.
MATRIX PROTEIN.
SEQUENCE 364 AA; 39645 MW;
                                                                       MM;
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Unit Release 3.1A John F. Collins, Biocomputing Research Ul Copyright (c) 1993-1998 University of Edinburgh, U.K Distribution rights by Oxford Molecular Ltd

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scale 0.367 46.283; Variance 17.007; Mean Statistics

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SUMMARIES

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17 49 59.8 1596 30 W31347 Rat tumour suppressor 7.49e+01 18 48 58.5 57.3 8 W88767 Yeast checkpoint cont 1.27e+02 20 46 56.1 208 3 W2664 Yeast checkpoint cont 1.27e+02 21 46 56.1 306 15 W3650 Porcine carboxypeptid 1.65e+02 22 46 56.1 349 20 W06174 Mature HCPB with Pell 1.65e+02 24 46 56.1 349 20 W06182 M041fied GCPB (D258) 1.65e+02 26 46 56.1 349 21 W13750 Carboxypeptidase B mu 1.65e+02 27 46 56.1 349 21 W13750 Carboxypeptidase B mu 1.65e+02 28 46 56.1 349 21 W13750 Carboxypeptidase B mu 1.65e+02 29 46 56.1 349 21 W13750 Carboxypeptidase B mu 1.65e+02 31 449 21 W13750 Carboxypeptidase B mu 1.65e+02 31 W13750 Carboxype
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ALIGNMENTS

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RESULT 1

ID W67035 standard; peptide; 12 AA.

AC W67035;

DT 15-DEC-1998 (first entry)

DE Tetanus toxin fragment (residues 1273-1284).

KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;

KW dendrimeric poly-lysine; epitope; tumour.

Clostridium tetani.

PN W09843677-A1.
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Query Match

Length 12; 36; DB Score 82; 100.08;

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100.0%;
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as host organism.
Disclosure; Fig 2; 50pp.
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GB-026832.
GB-006097.
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91-166115/23.
8; Q12121.
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P70345 standard; F
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27-NOV-1990;
28-NOV-1989;
17-MAR-1990;
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Terminator; v
Synthetic.
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                                                                                                                                                                            autoantigen; tumour antige therapy; genetic disease;
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Mismatches 0;
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  -03
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                                                                                                                                                             Tetanus toxoid protein fragment 1273-1284.
Microparticle, delivery; polymeric matrix; a
class II associated peptide; pathogen; gene
infection; downregulation; immune response.
              Mismatches
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Pred. No.
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  Pred.
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larity 100.0%;
Conservative
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ng peptide (6).
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Similarity 100.0%; 12; Conservative
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30-JUN-1998 (fi
Pan DR binding p
Pan DR binding p
DR locus.
Synthetic.
US5736142-A.
07-APR-1998.
14-SEP-1994; 305
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Tetanus
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78835;
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                                                                                or inducing MHC Class II mediated activation of T cells
Disclosure; Columns 33-34; 29pp; English.

The present sequence, a pan DR binding peptide, is capable of
binding antigen binding sites on MHC molecules, which are encoded
by most of the alleles of a DR locus. The peptide can be used to
inhibit or induce MHC Class II mediated activation of T-cells or
helper T-cells, which themselves mediate a CTL response. The
peptide can be used in mammals, especially humans, to inhibit
T-cell-mediated events involved in allograft rejection, allergic
responses and autoimmunity and as a vaccine adjuvant for enhancing
an immune response against an administered immunogen. The peptide
can be used with other immunogens to treat, e.g. prostate cancer,
hepatitis B, hepatitis C, AIDS, renal and cervical carcinoma,
lymphoma, CMV and condylyloma acuminatum.
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The (G+C) content of the synthetic gene is increased by 47% wrt the (G+C) content of the synthetic gene is increased by 47% wrt that in the content of the sequence. This eliminates six "terminator" regions which were found to be present in (A+T) rich regions. The terminators (termination/endo-nucleolytic processing/polyadenylation sites) were previously responsible for incomplete transcription of the mRNA. The elimination of these elements (using codon degeneracy) provided for successful expression in yeast of the tetanus toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 50,
5.29e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -03;
                        Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
                                                                       DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 82; DB 2;
. No. 5.29e-C
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fairweather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
(CYTE-) CYTEL CORP.
Alexander JL, Gaeta F, Grey HM, Sette A, S: WPI; 98-239154/21.
Peptides that bind to MHC molecules of all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tetanus toxin f
es for immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
n fragment C encoded by
vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WELL ) WELLCOME FOUNDATION LTD. Makoff AJ, Romanos MA, Clare JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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RESULT
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                                                                                                                                               Gaps
                                                                                                                                                                                                                              D-1; TTC; SOD:Tet451;
erve cell; stroke;
hypoxia-reperfusion;
                                                                                                      vaccine
                                                                          1 - or its fragments vaccine production.
                                                                                                                                              ÷
                                                                                              fragment, which may be sed as an antigen in va-
                                                                                                                                                                                     SSULT 6
W48909 standard; Protein,
W48909;
I 23-SEP-1998 (first entry)
E SOD-1/TTC hybrid protein.
W Chimeric; copper-zinc superoxide dismutase; SOD-1; TTC; SOD:
W Chimeric; copper-zinc superoxide dismutase; SOD-1; TTC; SOD:
W tetanus toxin fragment C; tetanus holotoxin; nerve cell; str
W neurological disorder; oxidative stress; brain hypoxia-reper
W epilepsy; Parkinson's disease; Huntington's disease.
OS Chimeric - Homo sapiens.
OS Chimeric - Clostridium tetani.
FH Key
I..163
//note= "SOD-1"
'-a .618
  tetanus
                                                                                                                                              Indels
                                                                                                                                Length 57
 of
                                                                                                                               e 82; DB 2; Len
1. No. 5.29e-03;
Mismatches 0;
 fragment
                                                                           toxin
for v
                                                                                              toxin fra
and used
                                                                          tetanus to
antigens
\mathbf{O}
                                                                                                                              Score 82;
Pred. No.
0; Mism
 the
               Closurian.
EP-209281-A.
21-JAN-1987.
27-JUN-1986; 305029.
28-JUN-1985; GB-016442.
(WELL) Wellcome Foundation Ltd.
Fairweather NF;
WPI; 87-015999/03.
N-PSDB; N70545.
Cloned DNA sequence coding for teta contg. epitope used to express anticontg. expressed in a transformed host, and a transformed host, and anticontg.
44
0
 all
                                                                                                                                • • • •
fragment and
                                                                                                                               Query Match
Best Local Similarity 100.08
Matches 12; Conservative
                                                                                                                                                           542
                                                                                                           against
573 AA;
Portion of B fragme
TT; vaccine.
Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 AA;
                                                                                                                                                           ggigndpnrdil
                                                                                                                                                                 production,
Sequence
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Sequence
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for
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conjugate(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use as vaccines.

Claim 1; Page 17; 20pp; English.

Epitopic peptides may be used with synthetic hapten derive a pathogen to generate an immune response to the pathogen. Peptides are recognised by numerous T-helper cell clones with context of a wide range of alleles of the human MHC. The peptides may be used in an antimalarial vaccine induciresponse to P.falciparium.

Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
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     Length
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me, is useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 78; DB 1; Len . No. 1.79e-02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         epitope.
vaccine; major histocompatibility
                               .. 0
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e 82; DB 33;
. No. 5.29e-03;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxin
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of immun
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J09262090-A.

O7-OCT-1997.

28-MAR-1996; 074227.

28-MAR-1996; JP-074227.

(DNIN ) DAINIPPON INK & CHEM INC.
WPI; 97-544153/50.
N-PSDB; T88370.

DNA encoding laminary pentose forming enscale recombinant production
Claim 1; Pages 7-9; 10pp; Japanese.
The DNA encoding the present sequence, Slaminary pentose forming enzyme, is usefrecombinant production of the enzyme.
Sequence 401 AA;
 Score 82;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78;
Pred. No.
1; Misma
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                                                                                                                                                                                                                             RESULT 7

ID R06308 standard; peptide; 12 AA.

AC R06308;

DT 04-DEC-1990 (first entry)

DE Tetanus toxin epitope.

KW Tetanus toxin; vaccine; major historing antimalarial.

KW antimalarial.

Synthetic.

PN EP-378881-A.

PN EP-378881-A.

PN 27-DEC-1989; 203318.

PR 17-JAN-1989; IT-019110.

PR 17-JAN-1989; IT-019110.

PR 17-JAN-1989; IT-019110.

PR 17-JAN-1989; IT-022409.

PR 17-JAN-1989; IT-019110.

PR 27-DEC-1989; IT-019110.

PR 27-DEC-1980; IT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33109 standard; Protein; 401 AA.
W33109;
28-JAN-1998 (first entry)
Streptomyces sp. laminary pentose
Laminary pentose forming enzyme; r
Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pentose
100.0%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.1%;
larity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..35
/label=
36..401
/label=
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                        Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
11; Conser
                                                                                                    gqigndpnrdil
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Query Match
Best Local S
Matches
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Best Local S
Matches 1
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                                                                                                       576
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localisation
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                                                                                                                                                              Sequence
                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388
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Matches
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                                                                                                                                                                                                                                                                                                                 activity
activity
activity
Example; Fig 2; 32pp; English.

The inventors claim a recombinant enzyme prepr. comprising beta-1,
3-glucanase or a mutant or variant and a vector contg. DNA encoding
it under the control of an exogenous promoter pref. lac UV5. The
it under the native beta-1, 3-glucanase gene isolated from
example uses the native beta-1, 3-glucanase gene isolated from
oerskovia xanthineolytica genomic DNA and expressed in pUV5-G1S.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lacking
                                                                                                                                                                                                                                                                                               transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein disulphide isomerase.
Yeast; protein disulphide isomerase; reticulum; localisation signal;
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                     ó
                                                                                                                                                                                                                                                                                                     of protease
     Length 401;
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                       Length 548
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein di:sulphide isomerase
                                                                                                                                                                                                                                                                                              - produced by and free of p
DB 25; LL.
1.37e+01;
                                                                                                                                                                                                                                                                                                                                                                                      e 51; DB 4; L
. No. 4.37e+01;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uchida K;
                     Mismatches
                                                                        R22197;
R22197;
R22197;
24-JUL-1992 (first entry)
Sequence encoded by beta-1, 3-glucanase ge
Recombinant enzyme; glucanase; pUV5-G1S.
Oerskovia xanthineolytica.
                                                                                                               ₽
                                                                                                                                                                                                                                                                       Slilaty
             4
                                                                                                                                                                                                                                                                                                                                                                                      Score 51;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTD.
', Tanaka H,
    Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                             beta-1,3-glucanase enzyme
ls with expression vectors
                                                                                                                                                                                                                                                                      Ä
                     ;
0
                                                                                                                                             1..36
/label= signal
444..448
/label= repeat
456..474
/label= repeat
488..492
/label= repeat
501..519
                                                                                                                                                                                                                      repeat
                                                                                                                                                                                                                           W09203557-A.
05-MAR-1992.
16-AUG-1991; CA0294.
17-AUG-1990; US-568869.
(CANA ) NAT RES COUNCIL CAN.
Shen SH, Chretien P, Bastien L
WPI; 92-096900/12.
N-PSDB; Q22957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Υ,
                                                                                                                                                                                                                                                                                                                                                                                     similarity 63.6%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant; endoplasmic refood processing.
Saccharomyces cerevisiae.
W09835049-A1.
13-AUG-1998.
06-FEB-1998; J00498.
07-FEB-1997; JP-038588.
(ORIY) ORIENTAL YEAST COLISHIIN, Matuo Y, Suzuki Y,
    62.2%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W69726;
16-NOV-1998 (first entry)
Saccharomyces cerevisiae p
Saccharomyces cerevisiae;
recombinant; endoplasmic r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein;
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) Okies...

1 N, Matuo Y, S

98-447246/38.

DB; V50470.
                                     14
            Similarity
                                              | ||||||||||QIGNDPNRDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                | :|||:||
QIGNDPNRDIL
                                    qnptdpnrdil
                                                                                                                                                                                                                                                                                                                                                                                                                       qndsdpnrnil
                                                                                                                                                                                                                                                                                                      cells
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W69726 stand
W69726;
16-NOV-1998
                                                                                                                                                                                                                                                                                              Recombinant
                     \infty
                                                                                                                                                                                                                                                                                                      E. coli cactivity
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sest Local s
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N-PSDB;
     Query Match
           Local
                                                                                                                                                                              region
                                                                                                                                                             region
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Best Loc
Matches
            Best Loc
Matches
                                    139
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The present sequence represents yeast (Saccharomyces cerevisiae)
The present sequence represents yeast (Saccharomyces cerevisiae)
Totelin disulphide isomerase (PDI). The present invention describes a biologically active recombinant yeast PDI, in which the endoplasmic reticulum localisation signal (His-Asp-Glu-Leu) at the C-terminal is defective or lacking, is produced by: (a) modifying a gene encoding the natural PDI by adding, deleting or substituting one or more bases in the part of all of the localisation signal fails; (b) inserting this modified gene into a suitable vector (such as the yeast expression vector YEPIGII); (c) transforming a host cell with the vector; (d) culturing the transformant at a pH near to neutrality (preferably at pH 6.5 to 8.0), and (e) isolating the PDI from the culture medium. PDI is used in the processing of foods such as ham, sausages, fish products and bean-curd (tofu). The modified PDI retains its biological activity by simple purification methods in high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 11

D R26174 standard; Protein; 526 AA.

C R26174;

T 04-FEB3-1993 (first entry)

T 04-FEB3-1993 (first entry)

W reast; isomerisation; catalyst; enzyme; disulphide bonds.

N 704197176-A.

Saccharomyces cerevisiae.

PR 322620.

PR 28-NOY-1990; 322620.

PR 28-NOY-1990; JP-322620.

PR 7070-10 TONER.

DR WPI; 92-288434/35.

DR WPI; 92-28841/35.

DR WPI; 92-288
                                                                                                                                                                                                                                            the
1 the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 522;
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W12662;
13-NOV-1997 (first entry)
Orange pectin methylesterase isoform L extension sequence Pectin methylesterase; PME; orange; de-esterified pectin; esterification; fruit juice; yoghurt; whey protein; casein protein stabilisation.
       use
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5.72e+01;
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4; Mismat
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Pred. No.
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larity 54.5%;
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larity 54.5%;
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sequence
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signal,
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QIGNDPNRDIL
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Disclosure, Fig The present seque
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Induces gealing in foodstuffs having less than 50% soluble solids
content, used for, e.g. preparation of foodstuff from fruits

Disclosure; Page 44; 29pp; English.

A composition has been developed which comprises a pectin methyl
cortiginate in situ from the other. The present sequence represents a PME
from Aspergillus aculeatus. Also described in the present invention are:

(1) a method of preparing the above composition by forming a mixture of
a PME and two PME substrates either one of which does not originate in
situ from the other; (2) a process comprising adding to a PME substrate,
a PME and another PME substrate, where neither PME substrate originates
in situ from the other; (3) a process of imparting stability to a
reaction medium comprising a PME substrate, by adding at least 1 PME and
a second PME substrate, where neither PME substrate originates in situ
from the other; (4) an aqueous system being in a solidified gel state
and having a soluble solids content of less than 50% w/w, where the
gelling has occurred by use of a high ester PME substrate; and (5) a
codstuff comprising or prepared from or by the invention. The methods
characterists are used in the preparation of foodstuff from materials.

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                                                                 R 14-0c.

A (DANI-) DANISCO co.

I Buchholt HC, Christensen land.

I Basmussen P, Thorsoe H;

NPSDB: 151740.

PT Stabilising protein in acidic soln. - by adding enzymatically de-esterified pectin, produced using pectin methylesterase

PS (laim 44; Page 75; 114pp; English.

CC This 220-amino acid polypeptide comprises an N-terminal extension sequence of orange pectin methyltransferase (PME). The extension cc is located N-terminally to the signal peptide of the PME (W12661) encoded by PME cDNA clone p034 (151739). The 64 kDa longer (L) isoform of PME is believed to be more heat stable than the 36 kDa shorter (L) isoform. Isoform S is believed to start the initial shorter (L) isoform. Isoform S is believed to start the initial compartability to a protein.

CC The 220-amino acid extension can be used to impart or increasing heat stability to a protein.

Sequence 220 AA;

CC 88; Score 49; DB 24; Length 220;

CC 88; Score 49; DB 24; Length 220;

CC 88; Score 49; DB 24; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 584 AA
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|lus aculeatus pectin met
| pectin methyl esterase;
                                           2-JUL-1996; E03051.
4-JUL-1995; GB-014438.
DANI-) DANISCO AS.
Suchholt HC, Christensen Tasmussen P, Thorsoe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus aculeatus.
WO9847391-A1.
29-OCT-1998.
24-APR-1998; IB0673.
24-APR-1997; GB-008278.
(DANI-) DANISCO AS.
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WPI; 98-583317/49.
N-PSDB; V64074.
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GQIGNDPNRDIL
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Aspergillus
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A (DANI-) DANISCO AS.

Buchholt HC, Christensen IMIE, Kreiberg JD, Nielsen C.,

Buchholt HC, Thorsoe H;

Rasmussen P, Thorsoe H;

Rasmussen P, Thorsoe H;

N-PSDB; T51739.

T stabilising protein in acidic soln. - by adding enzymatically de-esterified pectin. produced using pectin methylesterase

T de-esterified pectin. produced using pectin methylesterase (PME)

T de-esterified pectin. produced using pectin methylesterase (PME)

T de-esterified pectin. - by adding enzymatically de-esterified comprises a novel orange pectin methylesterase (PME)

T dolypeptide comprises a novel orange pectin methylesterase (PME)

C that can be obtained by expression of the PME coding sequence contained in NCIMB 40750 or of a CDNA clone (T51739) obtained from a norange fruit cDNA library. A longer isoform (see W12662) of the PME was also identified. Recombinant PME can be expressed in a contained method for de-esterifying a pectin. The de-esterified pectin is used in claimed methods for stabilising a protein in a codic environment (such as fruit juice, drinking yoghurt or drinks containing whey or milk proteins) without adversely affecting the viscosity of that environment. The recombinant enzyme can also be viscosity of that environment. The recombinant enzyme can also be viscosity of that environment. The recombinant enzyme can also be viscosity of that environment. The recombinant provel PME
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PME
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W12661;

W12661;

13-NOV-1997 (first entry)

Orange pectin methylesterase; PME; orange; de-esterified pectin;

Protein stabilisation.
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                      DB 37; Ld
7.49e+01;
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Pred. No. 7.49e+01;
4; Mismatches 2;
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Pred. No.
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Serrate-1; human jagged-1; H
cell fate; central nervous s
diagnosis; antibody.
Homo sapiens.
                                       59.8%;
larity 50.0%;
Conservative
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larity 50.0%;
Conservative
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47..584
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2-JUL-1996; E03051.
4-JUL-1995; GB-014438.
DANI-) DANISCO AS.
                                                                                                                                   69
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W05833 stand
W05833;
28-JAN-1997
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W09627510-A1.

12-SEP-1996.

07-MAR-1996; U03172.

R (TMCR) IMPERIAL CANCER RES TECHNOLOGY.

(UYIA ) UNIV YALE.

A (UYIA ) UNIV YALE.

I Lewis JH, Mann RS, Myat AM;
WPI; 96-425379/42.

N-PSDB, T40090.

Vertebrate Serrate protein and related DNA - used to treat or prevent malignancies characterised by increased Notch activity.

T Vertebrate Serrate protein and human serrate-2 (W05833) are ligands of the angle of the an
14..29
/label= Sig_peptide
185..229
/label= DSL
/note= "region of homology with Drosophila Delta
and Serrate, predicted to mediate binding
with Notch"
234..896
/label= ELR
/note= "epidermal growth factor-like repeat domain"
                                                                                                                                                   domain"
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/label= Partial_ELR
1068..1089
/label= Transmembrane_domain
1090..1218
/label= In+***
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265.299
/label= ELR2
300.339
/label= ELR3
340.377
/label= ELR4
378.415
/label= ELR6
454.490
/label= ELR9
529.566
/label= ELR9
529.566
/label= ELR1
709.747
/label= ELR12
748.785
/label= ELR13
786.823
/label= ELR14
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/label= P>
880..°
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 system disorders
                                                   1218;
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                                                 Score 49; DB 19; Louis Pred. No. 7.49e+01; 1; Mismatches 1;
    nervous
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or differentiation, partic. cancer, rand in tissue repair or regeneration. Sequence 1218 AA;
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                                                 Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 1.53 Seconds 79.635 Million cell updates/sec Tue Aug 17 16:00:27 1999; Run on:

not generated. output Tabular

>US-09-049-847-3 (1-12) from US09049847.pep 82 1 GQIGNDPNRDIL 12 Description: Perfect Score Title:

Sequence:

PAM 150 Gap 15 Scoring table:

10152877 residues 106580 seqs, Searched:

Post-processing

summaries Minimum Match 0% Listing first 45

Database

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

scale 0.379 Variance 42.182; Mean 15.008; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.		.05e-0	0.5e-0	.05e-0	.05e-0	.05e-0	05	.05e-0	.05e-0	.80e+0	.80e+0	.80e+0	.80e+0	.39e+0	.19e+0	.19e+0	.19e+0	.19e+0	.53e+0	.53e+0	.53e+0	.53e+0	.28e+0	.28e+0
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dę	Query Match	ţ	00	00.	00.	00.	00.	100.0	00.	00.	H	근	H	H	თ		۲.	7	۲.	ص	SO.	യ	Q	₹	寸
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Sequence 27, Application Sequence 2, Application Patent No. 5196194. Sequence 8, Application Sequence 10, Application Sequence 12, Application Sequence 12, Application Sequence 41, Application Patent No. 5183734. Patent No. 5183734. Patent No. 5183734. Sequence 7, Application Sequence 2, Application Sequence 3, Appli	17, APPLI 10. 5204446 10. 5183734 16, APPLI 20, APPLI 22, APPLI
US-08-222- US-08-222- 5196194-20 US-08-396- US-08-818- US-08-818- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-396- US-08-361- US-08-283-	S-U8-326 204446-4 183734-1 CT-US96- CT-US94- S-08-326
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ALIGNMENTS

FOR DELIVERY 2.0 Sequence 46, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
CORRESPONDENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER: EDISKette
COMPUTER: EDISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows Version 2.C
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELEFAX: Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS: AA 12 PRT; Application US/08787547 STANDARD; -46 US-08-787-547 46, Sequence XXXXXX RESULT DE

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Length 452;
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Pred. No. 1.05e-03;
0; Mismatches 0;
                                                                                                      A.A.
                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5571694th Glebe Road
CITY: Arlington,
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,228
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/618,312
FILING DATE: 27-NOV-1990
CLASSIFICATION: 435
                                                                                                     452
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                     PRT;
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELERAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
                                                                                                                                                                                                                                                                               K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
51770 MW; 1065961
                                                                                                                                                                                                                                                                                                           Neil
                                                                                                                                                                                                                    Sequence 4, Application US/08280228
Patent No. 5571694
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
                                                                                                                                                                                                                                                                Andrew J
Michael
effrey J
                                                                                                                                                                                                                                                            APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Nei
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       Application US/08280228
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Similarity 100.0%;
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Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Gaeta, Federico
APPLICANT: Alexander, John
APPLICANT: Alexander, John
TITLE OF INVENTION: Alteration of Immune Response Using Pan
TITLE OF INVENTION: Alteration of Immune Response O'SUBCURCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITX: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CITX: San Francisco
STREET: USA
ZIE: 94111-3834
COMPUTER: USA
ZIE: 94111-3834
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARDIAL STREET: O'S/08/305,871A
FILING DATE: 14-SEP-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: H-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
PROCESSERIES ATTORNEY, MATER: Bastian, MATER: Bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan
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Pred. No. 1.05e-03;
0; Mismatches 0;
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1.05e-03;
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REFERENCE/DOCKET NUMBER: 14137
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 576-0200
FORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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Pred.
0; M
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acids
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1426 MW; 6
                                          : peptide
1311 MW; 5
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larity 100.0%;
Conservative
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Similarity 100.0%;
12; Conservative
 amino
o acid
               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pep
SEQUENCE 12 AA; 1311
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Best Local Similarity 1
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Application US/07618312A
                         4, Application US/0761831
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MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPOPERATING SYSTEM: PC-I
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
larity 100.0%;
Conservative
                   Sequence 4, App. 1.
Patent No. 5389540
GENERAL INFORMATION:
                                                                                                           ADDRESSEE: 14th E
STREET: 2200 Clar
CITY: Arlington,
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                    linear
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/618,312A
FILING DATE: 19910516
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
APPLICATION NUMBER: GB 8926832.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e 82; DB 1; Le
. No. 1.05e-03;
Mismatches 0;
                       452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452
                                                                                                                                         APPLICANT: Fairweather Dr, Neil F
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: 14th Floor
STREET: 2200 Clarendon Boulevard,
CITY: Arlington,
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crawford Mr, Arthur R
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 510-51
TELEPHONE: 0101 703 8750400
TELEPHONE: 0101 703 8750400
TELEFAX: 0101 703 5253468
TELEX: 200797 NIXN UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
51797 MW; 1065526 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                       PRT
                                                                                                                 Makoff Dr, Andrew J
Romanos Dr, Michael A
Clare Dr, Jeffrey J
Fairweather Dr, Neil F
                                                                                      Sequence 2, Application US/07618312A
Patent No. 5389540
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
                                                                        Application US/07618312A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
0; M
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                      STANDARD;
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larity 100.0%;
Conservative
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52 AA;
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12; Consed
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                                                                                                                                                                                                                                                                                                         CURRENTING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/618,312A
FILING DATE: 19910516
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crawford Mr, Arthur R
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 510-51
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1. No. 1.05e-03;
Mismatches 0
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Patent No. 5443966
GENERAL INFORMATION:
APPLICANT: FAIRWEATHER, Neil Fraser
APPLICANT: MAKOFF, Andrew Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 452 AA; 51770 MW; 1065961 CN;
                                                                                                                                                     Clarendon Boulevard
                                                                                                                                                                                                                                                           : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: 14th Floor
                             ø
                                                             Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 0101 703 8750400
TELEFAX: 0101 703 5253468
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
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AMINO ACID
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DISMUTASE/TETANUS HYBRID PROTEIN
                                                                                Version
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Pred. No. 1.05e-03
0; Mismatches
                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Verentent APPLICATION DATA:
APPLICATION NUMBER: US/08/280,228
FILING DATE: 25-JUL-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/618,312
FILING DATE: 27-NOV-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                      CN;
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                                                                                                                                                                                                            FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                            ZIP: 22ZUL-*, 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5780024
GENERAL INFORMATION:
APPLICANT: Brown, Robert H.
APPLICANT: Francis, Jonathan W.
APPLICANT: Francis, Jonathan W.
APPLICANT: Hosler, Betsy A.
TITLE OF INVENTION: SUPEROXIDE DITITLE OF INVENTION: FRAGMENT C HY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
STREET: 225 Franklin Street
                                                                                                                                                                                MBER: GB 8926832
28-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5, Application US/08668381A
                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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51797 MW; 1065526
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                                                                                                                                                                                                                                                                                                                                            452 amino acids
ino acid
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                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE
FILING DATE: 28-NOV-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE
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Best Local Similarity 100.0%;
Matches 12; Conservative
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Arlington
         Virginia
                   COUNTRY: U.S.A. ZIP: 22201-4714
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SEQUENCE 452 AA;
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US-08-668-381A-5
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CITY: BC
STATE: N
COUNTRY:
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CITY:
STATE:
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Mismatches 0;
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571694th Glebe Road
                                         Road
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,337
FILING DATE: 29-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00943
FILING DATE: 20-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8914122.0
                                                                                                                                              ION DATA:
MBER: US/08/110,786A
23-AUG-1993 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; D
Pred. No. 1.
0; Mismatc
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T NUMBER: 117-134
I INFORMATION:
                                                                                                             compatible
rec-bos/Ms-bos
rn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil F
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDFP"
STREET: 1100 No. F"
              NUMBER OF SEXT.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08280228
Patent No. 5571694
GENERAL INFORMATION:
APPLICANT: Makoff Dr, Andrew J
APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil F
 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08280228
 Expression
                                                                                                                                                                                                                                                                      FILING DATE: 20 June 1989 ATTORNEY/AGENT INFORMATION:
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 816-400
TELEX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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51784 MW;
                                                                                                                                            CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                          NAME: Mary J. Wilson
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
Similarity 100.0%;
12; Conservative
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OPERATING SYSTEM: F
SOFTWARE: Patentin
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acid
                             ADDRESSEE: Nixon STREET: 1100 No. CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22201-4714
INVENTION: SEQUENCES:
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MOLECULE TYPE:
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US-08-557-
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Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECJ
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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             IBM PC compatible
LATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,381A
FILING DATE: 21-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/000,473
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00786/269001
TELECPHONE: 617/542-8906
TELECPHONE: 617/542-8906
TELECHONE: 617/542-8906
TELECHONE: 617/542-8906
TELECHOPATION FOR SEQ IT
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L.05e-03;
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~OMPUTER: IBM PC compatible
~TMG SYSTEM: PC-DOS/MS-DOS
~TMG SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/441,11.
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
TOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,9
                                                                                                                                                                                                                                                82;
No.
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Pred.
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ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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larity 100.0%;
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400 Garden
arden City
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ENCE 618 AA;
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CITY: G
STATE:
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:, 64th Floor
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FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-8655
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                         1256202 CN;
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    Score 50;
Pred. No. 1
4; Mismat
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEFAX: 516-742-4343
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
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. 5879664
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38
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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F: 405 Lexington Av
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carsten
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                                                                                                                                                                                          : protein
; 55937 MW; :
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58129 MW;
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larity 54.5%;
Conservative
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TITLE OF INVENTION: FU
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                              inear
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RY: United
10174-6401
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GENERAL INFORMATION:
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MOLECULE TYPE:
UENCE 504 AA;
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STREET: 40
CITY: New
STATE: New
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                                                                              5879664th America,
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SERRATE GENE AND METHCDS BASED THEREON
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                                                  Isomerase
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                                                                      ADDRESSEE: ...
ADDRESSEE: ...
STREET: 405 Lexinglow...
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                  Disulfide
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. No. 1.80e+01;
Mismatches 1
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                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                        SS
                                        Carsten Mailand
: Fungal Protein
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           US/08557122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08400159
Patent No. 5869282
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M..
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, SjappliCANT: Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08400159
                                                                                                                                                                                                                                                                                                                                                                                          Score Pred. 4; M
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                                                 Fungal
38
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                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 3052 amino ac
                                                                                                                                                                                                                                                                                                                                                             peptide
341596 N
         equence 26, Application Ustent No. 5879664
SENERAL INFORMATION:
APPLICANT: Hjort, CarstTITLE OF INVENTION: Fur NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                          61.0%;
larity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Henrique,
APPLICANT: Lewis, Ju
APPLICANT: Myat, Ann
APPLICANT: Fleming,
APPLICANT: Artavanis
APPLICANT: Artavanis
APPLICANT: Gray, Gray
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                  amino acid
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MOLECULE TYPE:
UENCE 3052 AA;
                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVNDPKKDVL
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US-08-400-159-6
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          Sequence
Patent No
GENERAL
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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 Length
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1.80e+01;
 DB 2; I
1.80e+01;
                                                                                                   530
                                                                                                                                                                                                                                                                                                                                                                                             KEFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICATION:
                                                                                                                                                                                                                                                                  LLE FORM:

LEE: Floppy disk

COREATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,122A

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 3°

REFERENCE/DOCKET NUM*

TELEPHONE:

TELEPHONE:

CORMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                         APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58796640 No. 58796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50;
Pred. No.
4; Misma
                                                                                                                                                                                US/08557122A
                                                                                                                                                            US/08557122A
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 50;
No.
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                                                                                                                                                                                                                                                            405 Lexington Avenue, New York
Score Pred.
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                                                                                                   STANDARD;
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59082 MW;
61.0%;
larity 54.5%;
Conservative
                                                                                                                                                                              Sequence 35, Application U
Patent No. 5879664
GENERAL INFORMATION:
APPLICANT: Hjort, Cars
TITLE OF INVENTION: FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%;
:y 54.5%;
servative
                                                                                                                                                            Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: li
MOLECULE TYPE:
UENCE 530 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conser
          Similarity 6; Conser
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                                        EIVNDPKKDVL
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QIGNDPNRDIL
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QIGNDPNRDIL
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CITY: N
STATE:
                                                                                                                                                            57
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  Query Match
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ID US-08-
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Matches
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388
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Matches
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US-08-198-
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDENCE ADDRESS:
SEE: Christensen O'Connor Johnson Kindness:
1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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ZIP: 98101-2347

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Le
Pred. No. 2.39e+01;
1; Mismatches 1;
                                                                                                                                                , Version
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   the Americas
                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
133810 MW; 7064054 CN;
                             STALL
COUNTRY: ULL
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMPUTER: IBM PC compatible
TAMPUTER: TRM PC COMPATIBLE
TAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08870593
Patent No. 5865338
GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Che(
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor a
SIREET: 1420 Fifth Ave., Suite 28
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
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Leslie
18,872
7326-
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                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
   of
                                                                                                                                                                                                                                                                                                                                                       FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 1218 amino acids
: 1155 Avenue
New York
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Similarity 77.8%;
7; Conservative
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JENCE 1218 AA
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-08-870-693-17
         STATE: N
COUNTRY:
ZIP: 1
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GNDPNRDIE
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Best Local S
Matches
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Pred. No. 4.19e+01;
4; Mismatches 2
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Cycle Checkpoint
APPLICATION NUMBER: US 08/198,446
FILING DATE: February 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         35,356
R: FHCR110798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FEB-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diana K.
3ER: 35,356
NUMBER: FHCR17537
                                                                                                                                                                                                                                                                                                                                                                       protein
yeast MEC2 protein
87015 MW; 3041193 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Christensen O'Connor
STREET: 1420 Fifth Ave., Suite 2
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08198446B
Patent No. 5674996
GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08198446B
                                                                                                                                                              NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
TELEFAX: 206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHOTELECOMMUNICATION INFORMATION:
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APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Groudine, Mark T
TITLE OF INVENTION: Cell Cy
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
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MOLECULE TYPE:
DESCRIPTION:
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CC TELEPHONE: 206-682-8100
CC TELEFAX: 206-224-0779
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 776 amino acids
CC TYPE: amino acids
CC TYPE: amino acid
TYPE: protein
CC MOLECULE TYPE: protein
SQ SEQUENCE 776 AA; 87015 MW; 3041193 CN;
Query Match
SQ SEQUENCE 776 AA; 87015 W; 3041193 CN;
CC MOLECULE TYPE: protein
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Db 289 GAVGEDAGREI 299
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Search completed: Tue Aug 17 16:00:34 1999
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Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.35 Seconds 119.724 Million cell updates/sec Tue Aug 17 16:02:46 1999; Run on:

not generated. output Tabular

>US-09-049-847-4 (1-13) from US09049847.pep 104 1 KFLAVWKITYKDT 13 Title: Description: Perfect Score: Sequence:

122810 seqs, 40068593 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing:

summaries Minimum Match 0% Listing first 45

pir60 1:pirl 2:pir2 3:pir3 4:pir4 Database:

scale 0.631 Mean 26.787; Variance 42.449; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

GNNY1P #type complete genome polyprotein (version 1) - human poliovirus 1 (strain	coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core protein P2-5b; core protein P2-5b; core protein P2-X; genome-linked protein VPg; probable proteinase P3-7c; protein P3-1b; protein P3-2; RNA-directed protein P3-2; RNA-directed	#formal_name human poliovirus 1 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change	A93258; A90800; A03897 A93258 Kitamura, N.; Semler, B.L.; Rothberg, P.G.: Larsen, G.R.	C.J.; Dorner, A.J.; Emini, E.A.; Hanecak, R. an der Werf, S.; Anderson, C.W.; Wimmer, E. 981) 291:547-553 tructure, gene organization and polypeptide ion of poliovirus RNA.	tes MUID:81220953 193258 Type genomic RNA 1-2207 ##label KIT1 rences GB:V01148; NID:9612 the amino acid sequenc	N.; Adler, C.J.; Rothberg, P.G.; Mon, S.G.; Wimmer, E. 0) 21:295-302 e-linked protein of picornaviruses. of poliovirus VPg by protein and R	A9 ty	P.G.; H 1. Acad.
RESULT 1 ENTRY TITLE	CONTAINS	ORGANISM DATE	ACCESSIONS REFERENCE #authors	#journal #title	#cross-referenc #accession P ##molecule_t ##residues ##cross-refe ##note	REFERENCE #authors #journal #title	#cross-referen #accession ##molecule_ ##residues ##note	REFERENCE #authors #journal

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ENT Coat proteins VP2 and VP3 and the RNA-directed RNA polyrelated to their counterparts in foot-and-mouth diseasing superfamily poliovirus genome polyprotein genome-linked protein; nucleotidyltransferase; phosphoprotein; polyprotein
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J. Biol. Chem. (1978) 253:5263-5266
Protein is linked to the 5' end of poliovirus phosphodiester linkage to tyrosine.
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Molecular cloning of poliovirus cDNA complete nucleotide sequence of the ces MUID:82060159
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Racaniello, V.R.; Baltimore, D.
Proc. Natl. Acad. Sci. U.S.A. (1
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genome polyprotein - human poliovirus 2 (strain W-2)
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  protein 1D; genome-linked protein VPg; nonstructural
  protein 2B; nonstructural protein 2C; nonstructural protein 2B; proteinase 2A; proteinase 3C; RNA-directed RNA
  polymerase (EC 2.7.7.48)
#formal_name human poliovirus 2
30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
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sference A34032

#authors Pevear, D.C.; Oh, C.K.; Cunningham Jubelt, B.

#journal J. Gen. Virol. (1990) 71:43-52

#title Localization of genomic regions sp mouse-adapted poliovirus type 2

#cross-references MUID:90155230

#accession A34032
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protein VP4; genome-linked protein VP9; nonstructural
protein 2B; nonstructural protein 2C; nonstructural protein
3A; proteinase (EC 3.4.-.-) 2A; proteinase (EC 3.4.-.-) 3C;
RNA-directed RNA polymerase (EC 2.7.7.48) 3D
#formal_name human poliovirus 2
31-Mar-1998 #sequence_revision 31-Mar-1988 #text_change
05-Jun-1998
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genome polyprotein - human poliovirus 2 (strain P712)
coat protein VP1; coat protein VP2; coat protein VP3; coat
protein VP4; core protein P2-3b; core protein P2-5b; core
protein P2-X; genome-linked protein VP9; protein P3-1b;
protein P3-2; protein P3-4a; protein P3-6a; protein P3-6b;
protein P3-9; proteinase P3-7c; RNA-directed RNA polymeras
(EC 2.7.7.48) P3-4b
#formal_name human poliovirus 2
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
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                                    Nomoto, A.; Omata, T.; Toyoda, H.; Kuge, S.; Horie, H.;
Kataoka, Y.; Genba, Y.; Nakano, Y.; Imura, N.
Proc. Natl. Acad. Sci. U.S.A. (1982) 79:5793-5797
Complete nucleotide sequence of the attenuated poliovirus
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Toyoda, H.; Kohara, ...
Toyoda, H.; Kohara, A.
Imura, N.; Nomoto, A.
J. Mol. Biol. (1984) 174:561-585
Complete nucleotide sequences of al
serotype genomes. Implication for
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coat protein VP1; coat protein VP2; coat protein VP3; coat
protein VP4; core protein P2-3b; core protein P2-5b; core
protein P2-X; genome-linked protein VP9; probable
proteinase P3-7c; protein P3-1b; protein P3-2; RNA-directed
RNA polymerase (EC 2.7.7.48) P3-4b
#formal_name human poliovirus 3
19-Feb-1984 #sequence_revision 03-Aug-1984 #text_change
26-Feb-1999
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1-2206 ##label ST1
#cross-references GB:K01392; NID:g332895; PID:g332896
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#residues 1-430,'F',432-863,'R',865-907,'A',909-2206
#experimental_source strain Sabin vaccine P3/Leon 12a[1]b
#note the authors translated the codon GAU for re
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##residues 1-2207 ##label TOY
##cross-references EMBL:X00595; NID:g61127; PID:e275415;
FICATION #superfamily poliovirus genome polyprotein
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VP2\
VP3\
VP1\
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coat protein VP1; coat protein VP2; coat protein VP3; coat
protein VP4; core protein P2-3b; core protein P2-5b; core
protein P2-X; genome-linked protein VPg; protein P3-1b;
protein P3-2; protein P3-4a; protein P3-6a; protein P3-6b;
protein P3-9; proteinase P3-7c; RNA-directed RNA polymeras
(EC 2.7.7.48) P3-4b
#formal_name human poliovirus 3
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
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                                                                       ts in foot-and-mouth dis
genome polyprotein
nucleotidyltransferase;
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lues 1-541,'Q',543-696,'M',698-1311,'E',1313-7
-references EMBL:X00596; NID:g61139; PID:g61140
N #superfamily poliovirus genome polyprotein
genome-linked protein; nucleotidyltransferase
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P3-7c #stat
ecule_type genomic RNA
idues 579-878 ##label STA
ss-references EMBL:V01540; NID:g61153; PID:g929811
erimental_source strain Sabin vaccine P3/Leon/37
Coat proteins VP2 and VP3 and the RNA-directed RNA
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   predicted #label P34\
#binding_site phosphoryl-RNA (Tyr) (c
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t protein P3-1b #status F
genome-linked protein V
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174:561-585
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                                                                     their counterparts in family poliovirus genom-linked protein; nucleo
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Toyoda, H.; Kohara, M
Imura, N.; Nomoto, Mnl. Biol. (1984)
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Complete nucleotide
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gene function and
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   ##molecule_type genomi
##residues 579-87
##cross-references EME
##experimental_source
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Nomoto,
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#accession S03822
##molecule_type gen
##residues 1--
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FEATURE

SUMMARY

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RESULT ENTRY TITLE

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nith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H
Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.;
Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle,
Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire,
Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Carus
A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.;
McDougall, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.;
Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D69182 #type complete
conserved hypothetical protein MTH62 - Methanobacthermoautotrophicum (strain Delta H)
#formal_name Methanobacterium thermoautotrophicum 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_c
                                                                                                                                                                                                                                                                                                                       ##residues 1-1040 ##label DEV ##cross-references GB:U39761; NID:g1079711; PID:g1079712
CLASSIFICATION #superfamily unassigned Ser/Thr or Tyr-specific kEYWORDS ATP
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sex myoblasts in Caer
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mplete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional and
                         #formal_name Caenorhabditis elegans
08-Feb-1996 #sequence_revision 08-Feb-1996
17-Mar-1999
A57638
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rotein kinase ATP-binding mo
#molecular-weight 118955 #c
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#length 250 #molecular-weight 28677 #c
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. No. 1.13e-
Mismatches
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                                                                                                                                    Devore, D.L.; Horvitz, H.R. Cell (1995) 83:611-620
An FGF receptor signaling p cell migrations of the se elegans hermaphrodites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70;
Pred. No.
1; Misma
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Pred. No. 3; Mismat
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#cross-references MUID:98037514
#accession D69182
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Complete genome
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larity 66.7%;
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Bacteriol.
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#accession A57638
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Best Local
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genome polyprotein - human poliovirus 3 (strain 23127)
coat protein VP1; coat protein VP2; coat protein VP3; coat
protein VP4; core protein P2-3b; core protein P2-5b; core
protein VP2-X; genome-linked protein VPg; protein P3-1b;
proteinase; RNA-directed RNA polymerase (EC 2.7.7.48)
#formal_name human poliovirus 3
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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A27245
REFERENCE
#authors Hughes, P.J.; Evans, D.M.A.; Minor, P.D.; Schild, Almond, J.W.; Stanway, G.
#journal J. Gen. Virol. (1985) 67:2093-2102
#title The nuclectide sequence of a type 3 poliovirus isc during a recent outbreak of poliomyelitis in Fin #accession A27245
#accession A27245
##molocular
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##residues 1-2206 ##label HUG
##cross-references GB:X04468; NID:g61112; PID:g61113
##CTOSS-references GB:X04468; NID:g61112; PID:g61113
FICATION #superfamily poliovirus genome polyprotein
COat protein; core protein; genome-linked protein; mucleotidyltransferase; phosphoprotein; protein; genome-linked protein; genom
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DNA polymerase III alpha chain (dnaE) homolog - Mycoplasma
genitalium (SGC3)
#formal_name Mycoplasma genitalium
17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
21-Aug-1998
H64228
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Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton,
R.A.; Fleischmann, R.D.; Bult, C.J.; Kerlavage, A.R.;
Sutton, G.; Kelley, J.M.; Fritchman, J.L.; Weidman, J.F.;
Small, K.V.; Sandusky, M.; Fuhrmann, J.; Nguyen, D.;
Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Hu, P.C.;
J.M.; Tomb, J.F.; Dougherty, B.A.; Bott, K.F.; Hu, P.C.;
Lucier, T.S.; Peterson, S.N.; Smith, H.O.; Hutchison III,
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#formal_name Mordacia mordax #common_name southern lan
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#formal_name Methanococcus jannaschii
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The primary structure of the hemisphere lamprey (Mord ces MUID:91248417
C.A.; Venter, J.C.
Science (1995) 270:397-403
The minimal gene complementerences MUID:96026346
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#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073
#title Methanococcus jannaschii.
#cross-references MUID:96337999
#accession F64503
##status preliminary; nucleic acid sequence not shown;
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##residues 1-255 ##label BUL
##cross-references GB:U67603; GB:L77117; NID:g1592220; PID:g159222;
##cross-references TIGR:MJ1632; PID:g1511593
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TTG
#superfamily hypothetical protein MJ1632
#length 255 #molecular-weight 29795 #c
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Score 61; DB 2; L. Pred. No. 4.00e+00; 3; Mismatches 4

Query Match
Best Local Similarity 46.2%;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

using Smith-Waterman algorithm protein - protein database search, MPsrch_pp

MasPar time 2.99 Seconds 122.872 Million cell updates/sec Tue Aug 17 16:03:24 1999; Run on:

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>US-09-049-847-4 (1-13) from US09049847.pep 104 1 KFLAVWKITYKDT 13 Iitle:
 Description:
 Perfect Score:
 Sequence:

PAM 150 Gap 15

Scoring table:

77977 segs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 Post-processing:

summaries

swiss-prot37
1:swissprot Database:

scale 0.713 Variance 38.609; Mean 27.515; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Length DB 1D Description Pred.	206 1 POLG_POLIM GENOME POLYPROTEIN [CO 7 73	208 1 POLH POLIM GENOME POLYPROTEIN CO 7 7	205 1 POLG_POL2W GENOME POLYPROTEIN [CO 2 11]	207 1 POLG_POL2L GENOME POLYPROTEIN [CO 2.11	209 1 POLG_POLIS GENOME POLYPROTEIN [CO 2 11	206 1 POLG_POL3L GENOME POLYPROTEIN CO 4 01	06 1 POLG_POL32 GENOME POLYPROTEIN [CO 1.05	040 1 EG15_CAEEL MYOBLAST GROWTH FACTOR 2.74	206 1 POLG_CXA21 GENOME POLYPROTEIN [CO 3.91	74 1 DP3A_MYCGE DNA POLYMERASE III, AL 9,20	49 1 GLB3_MORMR GLOBIN III.	38 1 MYSS_CHICK MYOSIN HEAVY CHAIN, SK 3.2	30 1 YX09_CAEEL HYPOTHETICAL 26.5 KD P 4.81	A_HELPY ALANYL-TRNA SYNTHETASE 4.81	74 1 POL1_HUMAN RETROVIRUS-RELATED POL 4.81	78 1 SYA_BACSU ALANYL-TRNA SYNTHETASE 4.81	32 1 XKDO_BACSU PHAGE-LIKE ELEMENT PBS 4.81	41 1 YNB0_YEAST HYPOTHETICAL 27.5 KD P 7.19	96 1 RMAR_YEAST MITOCHONDRIAL RIBOSOMA 7.19	5 1 EFIG_YEAST ELONGATION FACTOR 1-GA 7.19	67 1 KCOT_MOUSE COT PROTO-ONCOGENE SER 7.19	44 1 VP4 RTV11 VD4 CODE DECHETM
ć	Desc	OLIM G	OLIM G	OL2W GEN	OL2L GEN	POLIS G	POL3L G	POL32 G	CAEEL MYOB	CXA21 GENO	DNA	MORMR GLOB	MYOS	CAEEL HYPO	ELPY ?	HUMAN F	ACSU 7	BACSU	YEAST	YEAST MITO	YEAST ELON	OUSE COT	TV11 VP
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WP4_BTV10 MYSE_CHICK CAV3_HUMAN YCG8_YEAST YRAQ_ECOLI KCOT_HUMAN BUD5_YEAST SYA_MYCTU MYSB_MESAU MYSB_MESAU MYSB_RAT MYSA_RAT MYSA_RAT MYSA_RAT MYSA_HUMAN YS89_CAEEL DYHC_SCHPO YPC4_ECOLI RESD_BACSU PERE_HUMAN	LA_K
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                                                                                                                          0
                                                                                                                                                                             RESULT 2

ID POLH_POLIM STANDARD; PRT; 2208 AA.

AC P03300; Q84879; Q84880; Q89679;

DT 21-JUL-1986 (REL. 01, CREATED)

DT (1-OCT-1996 (REL. 34, LASI SEQUENCE UPDATE)

DT (15-DEC-1998 (REL. 37, LASI ANNOTATION UPDATE)

DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS

DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C

DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D

DE (EC 2.7.7.48)] (VERSION 2).

OS POLIOVIRUS TYPE 1 (STRAIN MAHONEY).

OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;

OC FUTEROVIRUS.
                                                                                                                                                                                                                                               CORE PROTEINS
                                                                                                                                                                                                                                                                                            PICORNAVIRIDAE
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VP2,
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PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE P.
SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CAUTION: SEE ALSO VERSION 1 OF THIS PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                 us cDNA and determination of the viral genome."; 78:4887-4891(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structures of poliovirus complexes with antiimplications for viral stability and drug des CURR. BIOL. 4:784-797(1994).

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE T Q/G SITES IN THE POLYPROTEIN. IT MAY BE A-1-SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF EACH OF WHICH IS COMPOSED OF ONE COPY EAC
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Mismatches
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GRANT R.A., HIREMATH C.N., FILMAN D.J., HOGLE J.M.;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 82060159.
RACANIELLO V.R., BALTIMORE D.;
"Molecular cloning of poliovirus cDNA complete nucleotide sequence of the vi PROC. NATL. ACAD. SCI. U.S.A. 78:4887-[2]
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MEDLINE; 85300512.
HOGLE J.M., CHOW M., FILMAN D.,
"Three-dimensional structure o
SCIENCE 229:1358-1365(1985).
[3]
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84.6%;
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TRANSFERASE; HIOL PROTEASE; MYRISTYLATION

PROTEZ (P1A). (P1B). (P1C). (P1C).

ORE PROTEIN; TRANSE HYDROLASE; THIOL P COAT PROTEIN VP4 (COAT PROTEIN VP2 (COAT PROTEIN VP3 (

EMBL; D00625; D1000971; ALT_SEQ.
PIR; A34032; GNNY2W.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C; 1
PFAM; PF00680; RNA_dep_RNA_pol; 1
PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
HSSP; P03299; 1POV.
POLYPROTEIN; COAT PROTEIN; CORE PROLYMERASE; HYDR

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3D

RNA POLYMERASE : SIMILARITY).

CORE PROTEIN 2B.
CORE PROTEIN 2C.
CORE PROTEIN 3A.
GENOME-LINKED PROTEIN VPG.
PICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE
MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).

PROTEASE 2A. CORE PROTEIN

69 340 578 879 1125 11454 11563 1746 1710

341 341 341 1029 1126 1455 1542 1747 1710

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                                                                                                                                                                                                                                                                                                                                                                               PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PICORNAVIRIDAE;
                                                                                                                                                                                                                                                         ESTLA STANDARD; PRT; 2205 AA.

D POLG_POLZW STANDARD; PRT; 2205 AA.

C P23069;
T 01-NOV-1991 (REL. 20, LASI SEQUENCE UPDATE)
T 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

T 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

E P2A TO P2C, P2A; GENOME-LINKED PROTEINS VP1 TO VP4; CORE PROTEIN

E P2A TO P2C, P2A; GENOME-LINKED PROTEIN VPG; PICCRNAIN 3C

ECC 2.7.7.48)]

S POLIOVIRUS TYPE 2 (STRAIN W-2).

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICCRNAVIRIDAE

C VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICCRNAVIRIDAE

SEQUENCE FROM N.A.

RX MEDLINE; 90155230.

RY

T.CCALLARLION OF GENOMIC REGIONS SPECIFIC for the attenuated, mouse-
RY

A GEN. VIROL. 71:43-52(1990).

C -: FUNTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

C -: FUNTION: P3C POLYPEPTIDE IS COMPOSED OF 60 ICOSAHEDRAL UNITS,

C -: FUNTION: P3C POLYPEPTIDE IS COMPOSED OF FOUR PROTEINS VP1, VP2

VP3, AND VP4.

C -: SUBDNIT: THE VIRUS CAPSID IS COMPOSED OF PROTEINS VP1, VP2

VP3, AND VP4.

C -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS

CC -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS

CC -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS

CC -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS

CC -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE POLITICE

C -: PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS

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A CYSTEINE PROTEASE.

F 60 ICOSAHEDRAL UNITS

ACH OF PROTEINS VP1, VI
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                                      2205;
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O1-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
O1-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CC
RC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYN
(EC 2.7.7.48)].
POLIOVIRUS TYPE 2 (STRAIN LANSING).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICC
ENTEROVIRUS.
[1]
SEQUENCE FROM N.A.
MEDLINE; 86115399.
LA MONICA N., MERIAM C., RACANIELLO V.R.;
"Mapping of sequences required for mouse neurovirulence of type 2 Lansing.";
"Mapping of sequences required for mouse neurovirulence of type 2 Lansing.";
"Napping of sequences required for mouse neurovirulence of type 2 Lansing.";
J. VIROL. 57:515-525(1986).
J. VIROL. SOLIFS IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PRC
-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRA
UND. AND WIDA.

-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF ONE COPY EACH OF PROTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CORE PROTEIN; TRANSFERASE;
SE; HYDROLASE; THIOL PROTEASE; M
COAT PROTEIN VP4 (P1A).
COAT PROTEIN VP2 (P1B).
COAT PROTEIN VP3 (P1C).
COAT PROTEIN VP1 (P1D).
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PICORNAIN 3C.
RNA-DIRECTED RNA POLYME
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PROTEASE (POTENTIAL).
PROIEASE (POTENTIAL).
MW; 36A83606 CRC32;
  ROTEASE (POTENTIAL); DA976BE8 CRC32;
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                                    e 85; DB 1;
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Mismatches
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2C.
3A.
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CORE PROTEIN 2
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PIR; A29507; GNNY5P.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C; 1
PFAM; PF00680; RNA_dep_RNA_pol; 1
PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
HSSP; P03299; 1POV.
POLYPROTEIN; COAT PROTEIN; CORE PRNA_DIRECTED RNA POLYMERASE; HYDR
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A GENBA Y., NAKANO Y., IMURA N.;

GENBA Y., NAKANO Y., IMURA N.;

T "Complete nucleotide sequence of the attenuated poliovirus Sabin 1

Strain genome.";

PROC. NATL. ACAD. SCI. U.S.A. 79:5793-5797(1982).

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE IHAT CLEAVES AT CERTAIN

C -!- FUNCTION: P3C POLYPEPTIDE IS COMPOSED OF 60 ICOSAHEDRAL UNITS,

EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,

VP3, AND VP4.

-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

C -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

C -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

C -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROCESS.

C -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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SE; HYDROLASE; THIOL PROTEASE; MY
COAT PROTEIN VP4.
COAT PROTEIN VP2.
COAT PROTEIN VP3.
COAT PROTEIN VP1.
CORE PROTEIN P2A.
CORE PROTEIN P2A.
CORE PROTEIN P2B.
CORE PROTEIN P2C.
CORE PROTEIN P3C.
RNA-DIRECTED RNA POLYMERASE P
MYRISTATE.
PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
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PO3301;

21-JUL-1986 (REL. 01, CREATED)

21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

[ 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; C

P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C

(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLY

E (EC 2.7.7.48)].

S POLIOVIRUS TYPE 1 (STRAIN SABIN).

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA SIAGE; PIC

ENTEROVIRUS.

(C ENTEROVIRUS.

I 1]

SEQUENCE FROM N.A.

(MEDLINE; 83299876.

(A MOMOTO A., OMATA T., TOYODA H., KUGE S., HORIE H., KAIAO)

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PIR; A03899; GNNY3P.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C; 1.
PFAM; PF00910; RNA_dep_RNA_pol; 1.
PFAM; PF00947; Pico_P2A; 1.
HSSP; P03299; 1POV.
POLYPROTEIN; COAT PROTEIN; CORE PFRNA-DIRECTED RNA POLYMERASE; HYDRC CHAIN
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X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-878.

SUBDITTED (MAR-1995) TO THE PDB DATA BANK.

C. !- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

C. !- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,

EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,

C. !- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

C. !- THE STRAIN SABIN VACCINE P3/LEON/37 IS SHOWN.

C. !- THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON/37 IS THE PAGE SABIN VA
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STRAIN=P3/LEON 12A[1]B;
MEDLINE; 83299239.
STANWAY G., CANN A.J., HAUPTMANN R., HUGHES P., CLARKE L.D.,
MOUNTFORD R.C., MINOR P.D., SCHILD G.C., ALMOND J.W.;
"The nucleotide sequence of poliovirus type 3 leon 12 alb: comparison with poliovirus type 1.";
NUCLEIC ACIDS RES. 11:5629-5643(1983).
                                                                                                                                                                                                                                                                                                                                                 PO3302;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
(EC 2.7.7.48)].
POLICYIRUS TYPE 3 (STRAINS P3/LEON/37 AND P3/LEON 12A[1]B).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=P3/LEON/37;
X MEDLINE; 84170338.
A STANWAY G., HUGHES P.J., MOUNTFORD R.C., REEVE P., MINOR P.D.,
A SCHILD G.C., ALMOND J.W.;
T. Comparison of the complete nucleotide sequences of the genomes of the neurovirulent poliovirus P3/Leon/37 and its attenuated Sabin vaccine derivative P3/Leon 12a1b.";
PROC. NATL. ACAD. SCI. U.S.A. 81:1539-1543(1984).
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                                                     e 85; DB 1; Le:
. No. 2.11e-05;
Mismatches 0;
    CRC32
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R.A., HIREMATH C.N., FILMAN D.J.,
                                                 Score 85;
Pred. No.
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HOGLE J.M.;
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FOLG_POL3L
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TO 1-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)

TO 1-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)

TO 5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS PLA TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C

E (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D

E (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D

E (EC 2.7.7.48)].

C VIRUSES, SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;

C ENTEROVIRGS.

NEDLINE; 87010550.

HUGHES P.J., EVANS D.M.A., MINOR P.D., SCHILD G.C., ALMOND J.W.,

A STANWAX G.;

T Tecent outbreak of poliomyelitis in Finland.";

J. GEN. VIROL. 67:2093-2102(1986).

C -!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

C -!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

C -!- FUNCTION: P3C POLYPEPTIDE IS COMPOSED OF 60 COCOSHEDRAL UNITS,

E BACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,

VP3, AND VP4.

PIW: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
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THIOL PROTEASE;
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COAT PROTEIN VP2.

COAT PROTEIN VP3.

CORE PROTEIN P2A.

CORE PROTEIN P2B.

CORE PROTEIN P2B.

CORE PROTEIN P2C.

CORE PROTEIN P3A.

GENOME-LINKED PROTEIN VPG
PICORNAIN 3C.

RNA-DIRECTED RNA POLYMERA

MYRISTATE.

PROTEASE (POTENTIAL).

PROTEASE (POTENTIAL).

PROTEASE (POTENTIAL).

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K -> A (IN P3/LEON 12A[1]

T -> A (IN P3/LEON 12A[1])

T -> A (IN P3/LEON 12A[1])
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EMBL; K01392; G332896; --
EMBL; X00925; G61155; --
PIR; A03900; GNNY4P.
PDB; 1PIV; 20-JUL-95.
PDB; 1VBA; 11-JUL-96.
PDB; 1VBB; 11-JUL-96.
PDB; 1VBB; 11-JUL-96.
PDB; 1VBC; 11-JUL-96.
PEAM; PF00073; rhv; 3.
PFAM; PF00680; RNA_dep_RNA_pol; PFAM; PF00947; Pico_P2A; 1.
PCAM; PF00947; Pico_P2A; 1.
PCAM; PF00947; Pico_P2A; 1.
POLYPROTEIN; COAT PROTEIN; CORE INA-DIRECTED RNA POLYMERASE; HYDI 30-STRUCTURE.
CHAIN 70 340 COAT CHAIN 879 1027 CORE CHAIN 1028 1124 CORE CHAIN 1125 1453 CORE CHAIN 1541 1562 GEN CHAIN 1541 1562 GEN CHAIN 1541 1563 1745 PICC CHAIN 1541 1563 1745 PICC CHAIN 1746 2206 RNA-LIPID 2 2 MYR.
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announgor send an email to license@isb-sib.ch).
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MYRISTATE (BY SIMILARITY).
PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
W; DD5809F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
EXTRACELLULAR DOMAIN CONTAINS 3 IG-LIKE DOMAINS.
         FAMILY
                                                                                                                                                                                                                                                                               TRANSFERASE;
THIOL PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STERN M.J.;
pathway is required for the
lasts in C. elegans hermaphro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE; 96069862.
DEVORE D.L., HORVITZ H.R., STERN M.J.;
"An FGF receptor signaling pathway is required for the migrations of the sex myoblasts in C. elegans hermaphic cell 83:611-620(1995).

CELL 83:611-620(1995).

THE GUIDANCE OF SEX MYOBLAST MIGRATION DURING GONG THE GUIDANCE OF SEX MYOBLAST GROWTH FACT.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACT.

THE IMMUNOGLOBULIN SUPERFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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       PEPTIDASE
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                                                                                                                                                                                                                                                                           GORE PROTEIN; TRANSFISE; HYDROLASE; THIOL PRODEIN VP4.
COAT PROTEIN VP2.
COAT PROTEIN VP3.
COAT PROTEIN VP1.
CORE PROTEIN P2B.
CORE PROTEIN P2C.
CORE PROTEIN P2C.
CORE PROTEIN P3A.
GENOME-LINKED PROTIPERORE PROTEIN P3A.
GENOME-LINKED PROTIPERORE PROTIPERORE PROTEIN P3A.
GENOME-LINKED PROTIPERORE PROTIPERORE PROTIPERORE PROTIPERORE PROTIPERORE PROTIPERORE (BY SIMILED PROTEIN PARTICULAR PARTICUL
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. No. 1.05e-03;
Mismatches 1
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L. 35, LAST SEQUENCE UPDATE)
L. 35, LAST ANNOTATION UPDAT
FACTOR RECEPTOR ELG-15 PREC
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   THE PROTEASE BELONGS
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                                                                                                                                                 EMBL; X04468; G61113; -.
PIR; A27245; GNNY27.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C;
PFAM; PF00548; Cys-protease-3C;
PFAM; PF00910; RNA_dep_RNA_pol;
PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
HSSP; P03302; 1PIV.
POLYPROTEIN; COAT PROTEIN; CORE
RNA-DIRECTED RNA POLYMERASE; HYD
                                                                                                                                                                                                                                                                             I PROTEIN; CO
POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHA
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9; Conservative
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Q10656;
01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
MYOBLAST GROWTH FAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLFATWRITYKDT
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1709
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                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
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: IN N1783; LOSS OF ACTIVITY.
: IN N1477TS; LOSS OF ACTIVITY
97C19793 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C) (P3C); RNA-DIRECTED RNA POLYMERASE
                                                                                                                                                                                                                   RECEPTOR
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P22055;
01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE
P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C
(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMEE
(EC 2.7.7.48)].
COXSACKIEVIRUS A21 (STRAIN COE).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORN
ENTEROVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1040
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                                                                         EMBL; U39761; G1079712; -.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00047; ig; 3.
PFAM; PF00069; pkinase; 1.
HSSP; P11362; 1FG1.
RECEPTOR; GLYCOPROTEIN; TYROSINE-PROTEIN KINASE; ATP-BTRANSFERASE; PHOSPHORYLATION; TRANSMEMBRANE; SIGNAL; IMMUNOGLOBULIN FOLD.
                                                                                                                                                                                                              MYOBLAST GROWTH FACTOR REENTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                 CYTOPLASMIC (POIENTIAL).

CYTOPLASMIC (POIENTIAL).

IG-LIKE DOMAIN.

IG-LIKE DOMAIN.

IG-LIKE DOMAIN.

IG-LIKE DOMAIN.

PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY.

POTENTIAL.

POTENTIAL.

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. No. 2.74e-02;
Mismatches 3
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Pred. No.
1; Misma
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ty 66.7%;
servative
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3; Conse
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FLAVWKITYKDT
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SEQUENCE
MEDLINE;
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MUTAGEN
SEQUENCE
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    FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L., NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M., TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S., TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S., The minimal gene complement of Mycoplasma genitalium."; SCIENCE 270:397-403(1995).

SCIENCE 270:397-403(1995).

-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN BNZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.

THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.

THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
M., ML.
S C.A., ML.
TICLER T.S.,
T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMPREY).
RATA; CEPHALASPIDOMORPHI
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MEDLINE; 91248417.

HOMBRADOS I., VIDAL Y., RODEWALD K., BRAUNITZER G
"The primary structure of the hemoglobins of a sc
lamprey (Mordacia mordax, Cyclostomata).";

BIOL. CHEM. HOPPE-SEYLER 372:49-56(1991).

-!- SUBUNIT: MONOMER.

PIR; S13460; S13460.

PROSITE; PS01033; GLOBIN; 1.

PROSITE; PS01033; GLOBIN; 1.

HSSP; P02208; ZLHB.

HSSP; P02208; ZLHB.

HEME; OXYGEN TRANSPORT; RESPIRATORY PROTEIN.

HEME; OXYGEN TRANSPORT; RESPIRATORY PROTEIN.

SEOUENCE 149 AA; 16508 MW; C50371DC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e 61; DB 1; Le.
. No. 1.40e+00;
. Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                     DB 1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORDACIA MORDAX (SOUTHERN HEMISPHERE LAMPREY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CEPH.
PETROMYZONTIFORMES; PETROMYZONTIDAE; MORDACIA.
                                                                                                                                                                                                                                                                                                                CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Mismatches
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                                                                                                                                                                                                                                                                                                                POLYMERASE; 28B83461
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Pred. No.
3; Misma
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Pred. No.
1; Misma
   J.E., SMALL
m R., SAUDEK
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larity 50.0%;
Conservative
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larity 70.0%;
Conservative
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TIGR; MG261; -.
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(REL. 18,
(REL. 18,
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KFLAVWKITYKD
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LAVWKITYKD
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01-MAY-1991
01-MAY-1991
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GLB3_MORMR
P21199;
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GLOBIN III.
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SEQUENCE.
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P13538;
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                                                 TO VESICULAR
                                                                                                                                                                                                                                                                                                                                                                                                MYRISTYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                       PROTEINS
                                                                          CERTAIN
       HUGHES P.J., NORTH C., MINOR P.D., STANWAY G.;

"The complete nucleotide sequence of coxsackievirus A21.";
J. GEN. VIROL. 70:2943-2952(1989).

-!- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESIC
MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAL
O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VI
VP3, AND VP4.

-!- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEIN
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                              SEIND
                                                                                                              \mathrm{VP1},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLAYTON R.A.,
ON G., KELLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOPLASMA GENITALIUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
MYCOPLASMATACEAE; MYCOPLASMA.
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(POTENTIAL).
(POTENTIAL).
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SE; HYDROLASE; THIOL PROTEASE; M
COAT PROTEIN VP4 (PlA).
COAT PROTEIN VP2 (PlB).
COAT PROTEIN VP3 (PlD).
COAT PROTEIN VP1 (PlD).
CORE PROTEIN P2A.
CORE PROTEIN P2A.
CORE PROTEIN P2B.
CORE PROTEIN P2C.
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PROTEASE (POT:
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PIR; A33373; GNNY21.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C;
PFAM; PF00680; RNA_dep_RNA_pol;
PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
HSSP; P03313; 1COV.
POLYPROTEIN; COAT PROTEIN; CORE
RNA-DIRECTED RNA POLYMERASE; HYD
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R.D., BULT C.J
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MEDLINE; 96026346.
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01-NOV-1997 (REL.
01-NOV-1997 (REL.
15-DEC-1998 (REL.
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TISSUE=PECTORALIS MUSCLE;
MEDLINE; 92041769.
MAITA T., MIYANISHI T., MATSUZONO K., TANIOKA Y., MATSUDA G.;
"The primary structure of skeletal muscle myosin heavy chain: III.
Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50 kDa, and 22 kDa fragments.";
J. BIOCHEM. 110:68-74(1991).
                                                                                                                                                                                                                                                                                                                                                      S., MATSUDA (chain: IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adult chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of subfragment-2 in adult chicken n.";
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TISSUE=PECTORALIS MUSCLE;
MEDLINE; 92041768.
KOMINE Y., MAITA T., MATSUDA G.;
"The primary structure of skeletal muscle myosin heavy chain: Sequence of the 50 kDa fragment of subfragment-1.";
J. BIOCHEM. 110:60-67(1991).
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 838-1938.
TISSUE=PECTORALIS MUSCLE;
MEDLINE; 92041770.
MAITA T., YAJIMA E., NAGATA S., MIYANISHI T., NAKAYAMA S., MA
"The primary structure of skeletal muscle myosin heavy chain:
Sequence of the rod, and the complete 1,938-residue sequence heavy chain.";
J. BIOCHEM. 110:75-87(1991).
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                                             IETAZOA; CHORDATA; VERIEBRATA; ARCHOSAURIA; AVI
GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS
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/ MAITA T., MATSUDA G.;
/ structure of skeletal muscle myosin heavy
the amino-terminal 23 kDa fragment.";
110:54-59(1991).
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MEDLINE; 89374803.
WAIANABE B.;
"Amino-acid sequence of the short subfragment-2 in skeletal muscle myosin.";
BIOL. CHEM. HOPPE-SEYLER 370:549-558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                              TANIOKA Y., KOMINE Y., of the myosin head."; U.S.A. 84:416-420(1987).
13, CREATED)
21, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
N, SKELETAL MUSCLE, ADULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.B.,
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MORIARITY D.M., BARRINGER K.J., YOUNG R.B.;
                                                                         SEQUENCE OF 1-205.
TISSUE=PECTORALIS MUSCLE;
MEDLINE: 92041767.
HAYASHIDA M., MAITA T., M
01-JAN-1990 (REL. 13, CRI
01-MAR-1992 (REL. 21, LAS
15-JUL-1998 (REL. 36, LAS
MYOSIN HEAVY CHAIN, SKELI
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORI
NEOGNATHAE; GALLIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete amino-acid sequeskeletal muscle myosin."; BIOL. CHEM. HOPPE-SEYLER
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MEDLINE; 89228549.
WATANABE B.;
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MEDLINE; 90121764.
WATANABE B.;
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                                                                                                                                                                                                                                                                                     SCIENCE 261:50-58(1993).

SCIENCE 261:50-58(1993).

SCIENCE 261:50-58(1993).

-!- FUNCTION: MUSCLE CONTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO F-- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

-!- SUBCELLULAR LOCATION: THICK FILAMENIS (MLC-2).

-!- SUBCELLULAR LOCATION: THICK FILAMENIS OF IHE MYOFIBRILS.

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKILATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKILATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

-!- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
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R PIR; PX0050; PX0051.

R PIR; A26821; A26821.

R PIR; A26821; A26821.

R PIR; S02082; S02082.

R PIR; S04501; S04501.

R PIR; S05515; S05515.

R PFAM; PF00063; myosin_head; 1.

R PFAM; PF000612; IQ; 1.

MYOSIN; MUSCLE PROTEIN; COILED COIL; THICK FILAMENT; ACTIN-BINDING; PFAM; PF00612; IQ; 1.

MYOSIN; MUSCLE PROTEIN; COILED COIL; THICK FILAMENT; ACTIN-BINDING; PFAM; PF00612; IQ; 1.

MYOSIN; MUSCLE PROTEIN; GOILED COIL; THICK FILAMENT; ACTIN-BINDING; PEPTAD REPEAT PATTERN; MULTIGENE FAMILY; 3D-STRUCTURE.

T DOMAIN : 837 GLOBULAR HEAD (S1).
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TAILPIECE (S2).
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WESENBERG
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LIGHT MEROMYOSIN (LAM).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
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MEDLINE; 93303624.
RAYMENT I., RYPNIEWSKI W
TOMCHICK D.R., BENNING M
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STRAIN=26695 / ATCC 700392;

MEDLINE; 97394467.

A TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
TOMB J.-F., WHITE O., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSCHMANN R.D., KETCHUM K.A., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
A LOFTUS B., RITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
A MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
The complete genome sequence of the gastric pathogen Helicobacter
T pylori.";
NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commenentities requires a license agreement (See http://www.isb-sib.ch/annowor send an email to license@isb-sib.ch).
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EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
[1]
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HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER
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2; Mismatches 3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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retrovirus
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CATALYTIC ACTIVITY: ATP + L-ALANINE + TRNA(ALA)
PYROPHOSPHATE + L-ALANYL-TRNA(ALA).
COFACTOR: BINDS A ZINC ION (BY SIMILARITY).
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA
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SEQUENCE FROM N.A.
MEDLINE; 87036922.
ONO M., YASUNAGA T., MIYATA T., I
"Nucleotide sequence of human enthe mouse mammary tumor virus ge
J. VIROL. 60:589-598(1986).
PIR; D24483; GNHUER.
PFAM; PF00075; rnaseH; 1.
PFAM; PF00078; rvt; 1.
PFAM; PF00652; integrase; 1.
PFAM; PF00665; rve; 1.
RANSP; P03366; 1HMV.
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Unit. .K. Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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>US-09-049-847-4 (1-13) from US09049847.pep 104 1 KFLAVWKITYKDT 13 Title: Description: Perfect Score: Sequence:

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residues seds, 54579741 179066 Searched

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Scoring

Post-processing:

summaries 08 45 Minimum Match Listing first

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l:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

scale 0.687 Variance 39.138; 26.892; Mean Statistics

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed; derived by analysis of the total score distribution. Pred. No. score grea and is der

SUMMARIES

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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIC
POLYPROTEIN (FRAGMENT).
HUMAN POLIOVIRUS 1.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NC
ENTEROVIRUS.
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=DAY 11 ISOLATE;
MEDLINE; 98411400.
KEW O.M., SUTTER R.W., NOTTAY B.K., MCDON QUICK L., PALLANSCH M.A.;
"Prolonged replication of a type 1 vaccinimunodeficient patient.";
J. CLIN. MICROBIOL. 36:2893-2899(1998).
EMBL; AF083931; G3617982; -.
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Pred. No.
2; Misma
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33505 MW;
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PICORNAVIRIDAE;

DNA STAGE;

SSRNA POSITIVE-STRAND VIRUSES, NO

CREATED)
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TYPE 1 (MAHONEY STRAIN).

OB4871
O84871;
O84871;
O1-NOV-1996 (TREMBLREL. O1, C1)
O1-NOV-1996 (TREMBLREL. O8, L2)
O1-NOV-1998 (TREMBLREL. O8, L2)
GENOME OF HUMAN POLIOVIRUS TYPE
(ONE OF TWO VERSIONS.).
POLIOVIRUS TYPE 1.
VIRUSES; SSRNA POSITIVE-STRAN

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Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1998 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
Q1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GENOME OF HUMAN POLIOVIRUS TYPE 1 (MAHONEY STRAIN).
(ONE OF TWO VERSIONS.).
POLIOVIRUS TYPE 1.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;
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SEQUENCE FROM N.A.
STRAIN=MAHONEY STRAIN;
MEDLINE; 82216986.
EMINI E.A., ELZINGA M., WIMMER E.;
"Carboxy-terminal analysis of poliovirus proteins: termination poliovirus RNA translation and location of unique poliovirus polyprotein cleavage sites.";
J. VIROL. 42:194-199(1982).
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STRAIN;
MEDLINE; 81220953.
KITAMURA N., SEMLER B.L., ROTHBERG P.G., LA
DORNER A.J., EMINI E.A., HANECAK R., LEE J.
ANDERSON C.W., WIMMER E.;
"Primary structure, gene organization and p
poliovirus RNA.";
NAIURE 291:547-553(1981).
[2]
SEQUENCE FROM N.A.
STRAIN=MAHONEY STRAIN;
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KITAMURA N., SEMLER B.L., ROTHBERG P.G.
DORNER A.J., EMINI E.A., HANECAK R., LE
ANDERSON C.W., WIMMER E.;
"Primary structure, gene organization a
poliovirus RNA.";
NATURE 291:547-553(1981).
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STRAIN=MAHONEY STRAIN;
MEDLINE; 82242310.
DORNER A.J., DORNER L.F., LARS "Identification of the initiat synthesis.";
J. VIROL. 42:1017-1028(1982).
EMBL; V01148; E9201; -.
PFAM; PF00073; rhv; 1.
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MEDLINE; 82060159.
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MEDLINE; 82060159.
RACANIELLO V.R., BALTIMORE D.;
"Molecular cloning of poliovirus cDNA and determination complete nucleotide sequence of the viral genome.";
PROC. NATL. ACAD. SCI. U.S.A. 78:4887-4891(1981).
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TYPE 1 (MAHONEY STRAIN)
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ANECAK R., LEE
                                                                                                                  STRAIN=MAHONEY STRAIN;
MEDLINE; 82216986.
EMINI E.A., ELZINGA M., WIMMER E.;
"Carboxy-terminal analysis of poliovirus poliovirus RNA translation and location of polyprotein cleavage sites.";
J. VIROL. 42:194-199(1982).
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STRAIN=MAHONEY STRAIN;
MEDLINE; 81220953.
KITAMURA N., SEMLER B.L., ROTHBERG P.G.
DORNER A.J., EMINI E.A., HANECAK R., LI
ANDERSON C.W., WIMMER E.;
"Primary structure, gene organization a
poliovirus RNA.";
NATURE 291:547-553(1981).
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[4]
SEQUENCE FROM N.A.
STRAIN=MAHONEY STRAIN;
MEDLINE; 82242310.
DORNER A.J., DORNER L.F., LARSEN G.R.,
"Identification of the initiation site
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Pred. No.
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POLICVIRUS TYPE 1.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES; SSRNA POSITIVE-STRAND VIRUSENTEROVIRUS.
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MEDLINE; 81013850.
KITAMURA N., WIMMER E.;
"Sequence of 1060 3'-terminal n determined by a modification of PROC. NATL. ACAD. SCI. U.S.A. 7
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synthesis.";
J. VIROL. 42:1017-1028(1982).
EMBL; V01148; E9174; -.
PFAM; PF00073; rhv; 3.
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SEQUENCE FROM N.A.
STRAIN=MAHONEY STRAIN;
MEDLINE; 82060159.
Nolecular cloning of poliovirus cDNA and determinatic complete nucleotide sequence of the viral genome.";
PROC. NATL. ACAD. SCI. U.S.A. 78:4887-4891(1981).
N [5]
P SEQUENCE FROM N.A.
C STRAIN=MAHONEY STRAIN;
X MEDLINE; 82216986.
A EMINI E.A., ELZINGA M., WIMMER E.;
"Carboxy-terminal analysis of poliovirus proteins: te poliovirus RNA translation and location of unique policy polyprotein cleavage sites.";
T Poliovirus A. 2194-199(1982).
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STRAIN=3786ALB96;
MEDLINE; 98312955.
FIORE L., GENOVESE D., DIAMANTI E., CATONE S., R.
IBRAHIMI B., KONOMI R., VAN DER AVOORT H.G., HOV.
SIMEONI P., AMATO C.;
"Antigenic and Molecular Characterization of Wilcausing Outbreaks of Poliomyelitis in Albania and Countries in 1996.";
J. CLIN. MICROBIOL. 36:1912-1918(1998).
EMBL; AJ007966; E1311747; -.
NON_TER
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. No. 2.19e-05;
Mismatches 0
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. No. 5.81e-05;
Mismatches 0
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
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SEQUENCE FROM N.A.
STRAIN=MAHONEY STRAIN;
MEDLINE; 82242310.
DORNER A.J., DORNER L.F., LARSEN (
"Identification of the initiation synthesis.";
J. VIROL. 42:1017-1028(1982).
EMBL; V01148; E9172; -.
PFAM; PF00073; rhv; 3.
PFAM; PF000548; Cys-protease-3C; 1
PFAM; PF00680; RNA_dep_RNA_pol; 1
PFAM; PF00910; RNA_dep_RNA_pol; 1
PFAM; PF00947; Pico_P2A; 1.
SEQUENCE 2221 AA; 248205 MW;
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of unique poliovirus
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Pred. No. 5.81e-05;
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SEQUENCE FROM N.A.
STRAIN=SABIN 1;
MEDLINE; 82216986.
EMINI E.A., ELZINGA M., WIMMER E.;
"Carboxy-terminal analysis of poliovirus propoliovirus RNA translation and location of polyprotein cleavage sites.";
J. VIROL. 42:194-199(1982).
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DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIC

DE GENOME OF HUMAN POLIOVIRUS, STRAIN SABIN 1

OS POLIOVIRUS.

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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATE POLYPROTEIN (FRAGMENT).
HUMAN POLIOVIRUS 1.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
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STRAIN=97-30515 (16/97/182);
MULDERS M.N., REIMERINK J.H.J.,
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Local Similarity 76.9%;
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STRAIN=SABIN 1;
NOMOTO A.;
SUBMITTED (APR-1988) TO E
EMBL; V01150; E9218; -.
PFAM; PF00073; rhv; 1.
SEQUENCE 302 AA; 33454
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MEDLINE; 82242310.
DORNER A.J., DORNER L.F.,
"Identification of the ir
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STRAIN=SABIN 1;
MEDLINE; 83299876.
NOMOTO A., OMATA T., T.
GENBA Y., NAKANO Y., I.
"Complete nucleotide si
strain genome.";
PROC. NATL. ACAD. SCI.
  98
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  HOVI T., KOOPMANS M.P.G.;
"A Sabin Vaccine-Derived Field Isolate of Poliovirus Ty
Displaying Aberrant Phenotypic and Genotypic Features,
Deletion in Antigenic Site 1.";
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF065158; G3511177; -.
                                                                                   Length
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No. 2.47e-04;
Mismatches 0
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No. 5.81e-05;
Mismatches 0
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Q98595;
Q1-FEB-1997 (TREMBLREL. 02, CREATED)
Q1-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIC PV2 POLYPROTEIN.
HUMAN POLIOVIRUS 2.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NC
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J. MOL. L.

[2]

SEQUENCE FROM N.A.

NOMOTO A.;

L. SUBMITTED (APR-1988) TO A.

SUBMITTED (APR-1988) TO A.

REMBL; X00595; E275415; -.

NR PFAM; PF00548; CYS-Protease-3C; 1.

DR PFAM; PF00548; CYS-Protease-3C; 1.

DR PFAM; PF00947; FNA_dep_RNA_pol; 1.

DR PFAM; PF00947; Pico_P2A; 1.

KW POLYPROTEIN; MEMBRANE.

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FT CHAIN

TO 340

POT

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TO 1454

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TO 1562

TO 1564

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TO 1567
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Pred.
4; M
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genomes. Implication for genetic 1
antigenic determinants.";
J. MOL. BIOL. 174:561-585(1984).
[2]
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MEDLINE; 84216300.
TOYODA H., KOHARA M., KATAOKA
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larity 69.2%;
Conservative
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HAUPTMANN R.,
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Mismatches 0;
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LAST ANNOTATION UPDAT
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Mismatches 0
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SEQUENCE FROM N.A.
MEDLINE; 84249506.
MINOR P.D., EVANS D.M.A., SCHILD G.C., FERG "Identification of an antigenic site in the poliovirus.";
REV. INFECT. DIS. 6:516-518(1984).
[2]
SEQUENCE OF 12-300 FROM N.A.
MEDLINE; 84249500.
ALMOND J.W., CANN A.J., MINOR P.D., REEVE I HAUPTMANN R., STANWAY G.;
"Nucleotide sequence from neurovirulent and type 3 poliovirus.";
"Nucleotide sequence from neurovirulent and type 3 poliovirus.";
REV. INFECT. DIS. 6:487-493(1984).
EMBL; M37321; G332982; -.
PFAM; PF00073; rhv; 1.
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POLIOVIRUS TYPE 3.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO ENTEROVIRUS.
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A.J.,
                                                                                POSITIVE-STRAND VIRUSES, NO
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STRAIN=LEON;

MEDLINE; 83141766.

MINOR P.D., SCHILD G.C., BOOTMAN J., EV.

REEVE P., SPITZ M., STANWAY G., CANN A.

MOUNTFORD R.C., ALMOND J.W.;

"Location and primary structure of a ma poliovirus neutralization.";

NATURE 301:674-679(1983).

EMBL; V01132; G929810; -.

EMBL; V01132; G929810; -.

PFAM; PF00073; rhv; 1.

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Pred. No.
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VIRUSES; SSRNA POSTUTEROVIRUS
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PRELIMINARY;
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Q84891
Q84891;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
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polioviruses.";
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Q84784

Q84784;

Q84784;

O1-NOV-1996 (TREMBLREL. 01, CREATED)

O1-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

COMPLETE SEQUENCE (STRAIN P3/119).

POLIOVIRUS TYPE 3.

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE:

[1]
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                                                         (FRAGMENT).
POLIOVIRUS TYPE 3.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA ENTEROVIRUS.
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Mismatches
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1.03e-03;
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Pred. No.
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Pred.
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STRAIN=P3/119;
MEDLINE; 85037944.
CANN A.J., STANWAY G., HUGHES P.J.
SCHILD G.C., ALMOND J.W.;
"Reversion to neurovirulence of the poliovirus vaccine.";
NUCLEIC ACIDS RES. 12:7787-7792(19)
FRAM; PF00073; rhv; 1.
PFAM; PF000548; Cys-protease-3C; 1.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
SEQUENCE 1628 AA; 182445 MW; 2.
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Q84793;

Q1-NOV-1996

Q1-NOV-1996

Q1-NOV-1998

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Mismatches
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2.63e-03;
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"Poliovirus type 3/Saukett: antigenic and st sequence variation in the capsid proteins."; VIROLOGY 199:228-232(1994).

EMBL; L23844; G388329; -.

EMBL; L23844; G388329; -.

PFAM; PF00073; rhv; 3.

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AA; 97326 MW; 1474D049 CRCE
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Q84792;
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O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O1, LAST SEQUENCE O1-NOV-1998 (TREMBLREL. O8, LAST ANNOTATIO PV3 POLYPROTEIN.
POLIOVIRUS TYPE 3.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO ENTEROVIRUS.
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984892;

01-NOV-1996 (TREMBLREL. 01, CREATED)

01-NOV-1998 (TREMBLREL. 03, LAST SEQUENCE

01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIC

CAPSID PROTEINS (FRAGMENTS).

POLIOVIRUS TYPE 3.

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NC
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NOMOTO A.;
SUBMITTED (APR-1985) TO EMBL/GENB EMBL; X00596; G61140; -.
PFAM; PF00073; rhv; 3.
PFAM; PF00548; Cys-protease-3C; 1 PFAM; PF00680; RNA_dep_RNA_pol; 1 PFAM; PF00910; RNA_helicase; 1.
PFAM; PF00947; Pico_P2A; 1.
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                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 84216300.
TOYODA H., KOHARA M., KATAOKA Y
NOMOTO A.;
"Complete nucleotide sequences"
                                                                                                                                                "Complete nucleotide sequences
genomes. Implication for geneti-
antigenic determinants.";
J. MOL. BIOL. 174:561-585(1984)
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STRAIN=SAUKETT COP;
MEDLINE; 94160574.
HUOVILAINEN A., KINNUNEN L.,
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9; Conserv
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KFLAVWKITYKDT
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                                                                                                                             NO DNA
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  Mismatches
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Q84896,
Q84896,
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE
Q1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIO
CAPSID PROTEINS (FRAGMENTS).
VP-1.
VOLIOVIRUS TYPE 3.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO
ENTEROVIRUS.
[1]
SEQUENCE FROM N.A.
STRAIN=SAUKETT H;
MEDLINE; 94160574.
HUOVILAINEN A., KINNUNEN L., POYRY T., LAAHOVI T.;
"Poliovirus type 3/Saukett: antigenic and
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Matches 9; Conservative
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Collins, Biocomputing Research 998 University of Edinburgh, U. rights by Oxford Molecular Ltd Release 3.1A John F. Copyright (c) 1993-19 Distribution

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ALIGNMENTS

W67036,
W7 Tetaus toxin; vaccine; antibody; carbohydrate peptide conjugate;
Poliovinus m1290,
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W7 Tetaus toxin; vaccine; antibody; carbohydrate peptide conjugate;
W67036,
W7 1987; US-041726,
W7 1987; US-041726,
W7 1989; ED1922.
W7 1989; W67031,
W7 1989; W7 1989;
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W7 19 AA 13 standard; peptide; RESULT 1 ID W67036 ID AC DI DE

Length Score 104; DB 36; Pred. No. 6.52e-04; Query Match Best Local Similarity 100.0%;

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/label= P4
70..341
/label= VP2
342..579
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580..881
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30-NOV-1983; 402310.
30-NOV-1982; FR-020115.
29-JUN-1983; FR-010778.
01-JAN-1989; EP-102888.
(INSP ) INST PASTEUR.
(GIRA/) GIRARD M.
Girard M, Van der Werf SWPI; 84-147943/24.
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Polio virus.
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Q
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The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an antibody purified from biological fluid or cells of organisms administered with the carbohydrate peptide conjugate, and (2) a diagnific comprising antigen-specific antibodies elicited by immunisation the carbohydrate peptide conjugate. The peptide conjugate, antibody diagnosis kit are used to provide pharmaceutical compositions and vaccines against tumours. These can be used to support an immune resagainst viral infections caused by hepatitis virus, HIV or cytomegal virus. They can be used to enhance immune responses, especially B-
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from poliovirus VP-1 protein peptide conjugates and oligomers,
eful in vaccines and diagnosis.
sclosure; page 3; 53pp; English.
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No.
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Carbohydrate peptide conjugate used as with dendrimeric poly-lysine enabling covalently attached
Example 5; Page 32; 55pp; English.
The invention relates to a new carbohy
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VP-1 capsid protein
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Poliovirus VP-1 capsid pr
Poliovirus; VP-1 capsid;
Poliovirus
EP-323861-A.
12-JUL-1989.
30-NOV-1983; 102888.
30-NOV-1982; FR-020115.
(INSP) Institut Pasteur.
Girard M, van der Werf S;
WPI; 89-200752/28.
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W09843677-A1.
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(INSP.) INST PASTEUR.
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rne sequence is that of amino acids 23-128 of policapsid polypeptide (see N90247). The peptide is rantibody C3. It is useful as a reagent for detectianti-poliomyelitis antibodies, and as a component It contains the necessary antigenic determinants, enough to be synthesised chemically.
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Sequence encoded by a full-length of the plasmid pvR106.
Poliovirus; picornavirus; vaccine; Human poliovirus.
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e of a peptide recognised k
irus capsid; VP-1 structura
; diagnosis.
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a peptide (P401)
e against C and )
VP-1 structural;
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AC WE
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28-OCT-1982.

P 28-OCT-1982.

P 28-OCT-1982.

P 12-NOV-1981; 320525.

R 20-APR-1981; US-255879.

R 20-APR-1981; US-255879.

R 12-NOV-1981; US-350525.

R 20-APR-1981; US-350525.

R 20-APR-1981; US-350525.

R 20-APR-1981; US-350526.

R 20-APR-1981; US-255879.

R 20-APR-1981; US-255879.

R 20-APR-1981; US-250526.

R 20-APR-1981; US-255879.

R 20-APR-1982.

R 20-APR-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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H 4-JUL-1992 (first entry)

E True type 3 poliovirus protein from LED3.

RNA virus; error reduction.

S Poliovirus.

N W09203538-A.

N W09203538-A.

N W09203538-A.

D 55-MAR-1990; US-570000.

R 20-AUG-1990; US-569916.

R R Canhiello V, Tatem JM, Weekslevy CL;

R PPSDB; O22965.

R New vaccine against infectious polio-virus comprises RNA virus.

T for producing RNA virus cDNA and viable RNA virus.

T for producing RNA virus cDNA directs the prodn. of a viable collovirus obtd as in Q22965. The cDNA directs the prodn. of a viable collovirus which is phenotypically similar to the source virus.

C The full length cDNA in pLED3 was infectious. In vitro consocribition of pLED3 cDNA using T7 RNA polymerase produced contrass which possessed several erroneous amino acids. The RNA viruses are used in vaccines against polio. The screening method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e 87; DB 5; Len
l. No. 5.31e-02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 2206 AA
                                                                                                                                                                                                              4(p(63)
/label= 3b
1031..1127
/label= 5b
1128..1456
/label= X
1457..1543
/label= 1b
1544..1565
/label= VPg
1566..1748
/label= 2
1749..2209
/label= 4(P(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 83.7%;
Local Similarity 84.6%;
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694
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| KFLAVWKITYKDT
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Best Local S
Matches 1
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R22210;
                   protein
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Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial diagnosing anti-microbial agents for treatment of bacterial claim 12; Page 350; 483pp; English.

Claim 12; Page 350; 49 proteins of particular the proteins of the invention can be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal inplantation of in-dwelling devices or other than by the inplantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae protein of unknown function.
Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis.
Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ig
can be used during amplification of the source virus for vaccinal prodn. to ensure maintenance of C at position 2493 in the viral genome i.e. increasing the attenuation. The new prod. overcomes the problem of errors introduced during replication of ss RNA, which is much higher than for ds DNA.

Sequence 2206 AA;
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O
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l. No. 2.41e+01;
Mismatches 2;
                                                                                                                                                                                                        ·, O
                                                                                                                                                                          e 79; DB 4; L
. No. 3.97e-01;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholas
                                                                                                                                                                          Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAM PLC.
Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOY/#JU07.
20-NOV-1997, U07950.
14-MAY-1996; US-017670.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEECHAM FLC.
'SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
2; M
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larity 60.0%;
Conservative
                                                                                                                                                                       76.0%;
larity 69.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                                         691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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Black MT, HC.
Stodola RK;
"PI; 98-008793/01.
"PI; 98-008793/01.
"PI; 98-008793/01.
                                                                                                                                                                                                                                                                  klfamwritykdt
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KFLAVWKITYKDT
                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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20-NOV-1997.
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W38579 stand
W38579;
06-NOV-1998
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                                                                                               S Thermus I lavus.

BP-884384-A2.

16-DBC-1996.

17-DBC-1996.

18-MAY-1997; JP-122635.

18-MAY-1
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WO9630387-A1.

WO9630387-A1.

WO9630387-A1.

WO9630387-A1.

WO9630387-A1.

Cha T. Spacte R;

R (AVIR-) AVIRON.

I Cha T. Spacte R;

R WPI; 96-45525/45.

R N-PSDB; T41418.

Toledo strains, used to develop prods. for the diagnosis, prevention and treatment of human CMV infections

Toledo strains J Page 85-88; 150pp; English.

Novel protein UL150 (W05519) is the product of an open reading frame found in a novel nucleic acid (T41418) isolated from the Toledo strain of human cytomegalovirus (HCMV). UL150 and other novel (see also W05502-20) and known (see also W05500-01) proteins of the Toledo strain, as well as new proteins (see also W05521-24).

Tom HCMV Towne, can be produced in transformed host cells and used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l - from Towne and
diagnosis, prevention
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                                                   glucan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
01-MAR-1999 (first entry)
Thermus flavus amylomaltase.
Thermus flavus; amylomaltase; heat resistant; cyclic gintramolecular transglycosylation; alpha-glucan; food. Thermus flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 3.04e+01;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
strain UL150 protein (clone tol.21)
vaccine; diagnosis; UL150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61;
Pred. No. 3
5; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 AA
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Local Similarity 41.7%;
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
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W05519;
15-JAN-1997 (first e
HCMV Toledo strain UI
CMV; HCMV; vaccine; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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1 KFLAVWKITYKD
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Matches
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Example 1; Page 86-87; 141pp; English.

This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                          Gaps
                                                      infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gap
                                                                                                                                                                                                                                                                                                                                                            detection;
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O
                                        for
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                      HCMV. They may be corresponse of an in
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                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                        Length
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W71868;
06-JAN-1999 (first entry)
Amino acid encoded by prostate tumour clone J1-1
Prostate; cancer; tumour; vaccine; immunogen; cl
Homo sapiens.
W09837093-A2.
27-AUG-1998.
25-FEB-1998; U03492.
09-FEB-1998; US-806099.
01-AUG-1997; US-904804.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-609886/51.
N-PSDB; V61200.
                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e 59; DB 35;
No. 4.83e+01;
Mismatches 1
                                                                                                                      e 61; DB 19;
. No. 3.04e+01;
Mismatches 2
                                                          immune
surface glycoproteins that are immunogenic tissue tropism, or may influence the immune individual.
                                                                                                                                                                                                                                                                                                                                          J1-17
                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                              one
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Pred.
3; M
                                                                                                                         Score
Pred. ]
2; M
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                                                                                                                                                                                                                                                                                                                Us-DEC-1998 (first entry)
Prostate tumour specific gene (Prostate tumour specific gene; therapy.
                                                                                                                                                                                                                                                                                          315
                                                                                                                       58.7%;
larity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 55.6%; 5; Conservative
                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
W09837418-A2.
27-AUG-1998.
25-FEB-1998; U03690.
09-FEB-1997; US-806596.
01-AUG-1997; US-904809.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI; 98-480805/41.
                                                                                                                                                                                           414
                                                                                                                                         Similarity 7; Conser
                                                                                                                                                                                                                           ۲-1
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                                                                                                                                                                                                                                                                                          standard;
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FLAVWKITY
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71868 stand
71868;
5-JAN-1999
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08-DEC-1998
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Best Local
                                                                                                                           Match
                                                                                                                                          Local
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                                                                                                                                                                                                                                                                          RESULT 10
W69384
AC W69384;
DT W69384;
DT W69384;
DT O8-DEC-
DE PROSTAT
KW Therapy
OS HOMO SA
PN W098374
PD 27-AUG-
PR 09-FEB-
PR CORI-)
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Detecting a curry prostate cancer

Example 10; Page 89-90; 104pp; English.

This sequence represents the human PS112 protein derived from various gene specific clones isolated from a prostate library and is used in a gene specific clones isolated from a prostate library and is used in a novel method of detecting the presence of a target PS112 polynucleotide in a test sample. The method can also be used to detect mRNA of PS112 ir a test sample. The method can be used for diagnosis of prostate cancer, as the presence of PS112 is an indicator of prostate cancer. Antibodies as the presence of PS112 is an indicator of prostate cancer. Antibodies
                                                                                                                                                                             0
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                                                                                    subtracting tissue cDNA
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             prostate proteins cancer
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                                                                            Was
                                                 prostate
be used a
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Polypeptides comprising immunogenic portions of prostate proused in a vaccine for the treatment of prostate cancer Example 1; Page 81-82; 130pp; English.

The present sequence is an immunogenic portion of a prostate protein. The immunogen, or the DNA encoding it, can be used vaccine for the treatment of prostate cancer. The immunogen isolated from a prostate tumour cDNA library obtained by sublibrary.
                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                    Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aureus.
immunological response;
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                                                                                                                                                                                                                                                                                                                             diagnosis;
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W21898;
W21898;
11-SEP-1997 (first entry)
3 Alanyl-tRNA synthetase from Staph. aureus.
W tRNA synthetase; Escherichia coli; immunologica.
W bacterial infection; adherence; damaged tissue; wor vaccine; skin; protection.
Staphylococcus aureus.
Staphylococcus aureus.
                                                                                                                                               e 59; DB 36; Le
l. No. 4.83e+01;
Mismatches 1;
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. No. 4.83e+01;
Mismatches 1;
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Russell
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3; M
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W54425;
15-SEP-1998 (first entry)
Human PS112 protein sequence from Prostate; disease; PS112 gene; diment; antibody.
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16-APR-1998.

08-OCT-1997; U18290.

08-OCT-1996; US-727688.

(ABBO ) ABBOTT LAB.

Cohen M, Friedman PN, Gordon J, Kratochvil JD, Roberts-Rapp L, RWPI; 98-240838/21.
                                                                                                                                                                                                                                                                                                                                                                                                     "partial
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/label= PS112
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larity 55.6%;
Conservative
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larity 55.6%;
Conservative
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A (SMIN ) SMIN ) SMIN DELIANDED STATES A (SMIN ) SMIN ) SMIN ) SMIN ) SMIN ) SMIN ) Hodgson JE, Lawlor EJ; WRI, 97-365935/34.

N-PSDB; T73696.

The process alanyl-tRNA synthetase from Staphylococcus aureus WCOB 29 - useful for protection against bacterial infections claim 1; Fig 2; 35pp; English.

The present sequence represents a novel alanyl-tRNA synthetase protein from Staphylococcus aureus strain WCUB29 (NCIMB 40771), which is related by amino acid sequence homology to Escherichia coli alanyl tRNA synthetase. Vectors comprising the DNA (or polynucleotides having at synthetase. Vectors comprising the DNA (or polynucleotides having at least 70 % identify to it) can be used for the recombinant production of the enzyme. The enzyme or its related DNA (through gene therapy) is used to induce an immunological response in a mammal to generate carticolates are protect against disease. The antibodies protect against crisue, including wounds in skin or connective tissue caused by mechanical, chemical or thermal damage or by implantation of in-dwelling devices, or wounds in the mucous membranes. Artagonists are used to inhibit the enzyme, especially to prevent adhesion of bacteria to devices or to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds, or to block tRNA synthetase protein mediated mammalian tyrosine kinase. Analysing a sample for the presence of the enzyme (or a polypeptide having at least 70 % identity to it) is used for a diagnostic process.
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s sequence represents a human heart calveolin protein. This protein is sequence represents a human heart calveolin protein. This protein is be used for prophylaxis and treatment of diabetes, obesity, cancer, criosclerosis and muscular dystrophy. Calveolin can also be used for intifying compounds which can promote or inhibit its activity.
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ystrophy; inhibitor.
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6.07e+01;
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.No. 7.62e+01;
Mismatches 1
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eart caveolin protein.
1; human; heart; prophylaxis; treatment arteriosclerosis; muscular dystrophy;
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Pred. No.
6; Misma
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Pred. No.
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diabetes,
17-JAN-1997; 300309.
19-JAN-1996; GB-001099.
30-OCT-1996; GB-022617.
(SMIK ) SMITHKLINE BEECHAM PLC.
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03-JUL-1997; 177496.

09-JUL-1996; JP-179666.

(TAKE) TAKEDA CHEM IND LTD.

WPI; 98-267126/24.

N-PSDB; V11143; V11147.

New human heart caveolin prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.8%;
larity 25.0%;
Conservative
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larity 55.6%;
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W40495 standard; Protein;
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and muscular dystrophy
Claim 1; Fig 1; 25pp;
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151 AA:
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Caveolin; human;
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identifying
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Homo sap
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JOB228782-A.

JOB228782-A.

JOB228782-A.

JOSEP-1996.

18-SEP-1994; JP-248700.

RATS/) MATS/NAGA T.

(DENK ) TDK CORP.

WPI; 96-459147/46.

N-PSDB; T46127.

Magnetic particles formed in magnetic microbe AMB1, useful for stable prepn. of proteins

Claim 2; Page 9-11; 17pp; Japanese.

The magA protein binds to an organic membrane covering fine magnetic particles formed in the magnetic microbe AMB1, useful for stable protein binds to an organic membrane covering fine magnetic particles formed in the magnetic microbe AMB-1. The magnetic microbe can be used for the stable prepn. of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
RESULT 15

WO1520 standard; Protein; 434 AA.

AC W01520;

DI 28-FEB-1997 (first entry)

DE MayA protein.

KW magA; magnetic; microbe; protein preparation; organic membrane.

SM Magnetospirullum sp.

FH Key

7.380

7.380

FT region

7.380

FT region

7.380

FT Albel= hydrophobic_region

FN JO8228782-A.

PD 10-SEP-1995; 263487.

PR (APSE)

RATSONAGA T.

PA (DENK) TDK CORP.

DR WPI; 96-459147/46.

PT magnetic particles formed in magnetic membrane - covering fine magnetic particles formed in magnetic microbe AMB1, useful for proper proper of proteins

PT magneticles formed in magnetic membrane covering fine magnetic complements be seally binds to an organic membrane covering fine magnetic complement of proteins.

PT magneticles formed in the magnetic microbe AMB1, useful for particles formed in the magnetic microbe AMB1. The magnetic microbe can be used for the stable prepn. of proteins.
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Pred. No. 7.62e+01;
2; Mismatches 2;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 1.57 Seconds 83.835 Million cell updates/sec Tue Aug 17 16:04:36 1999; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

output not generated. Tabular

>US-09-049-847-4 (1-13) from US09049847.pep 104 1 KFLAVWKITYKDI 13

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15

Scoring table:

106580 seqs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

scale 0.295 Mean 18.363; Variance 62.160; Statistics:

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APPLICANT:
APPLICANT:
APPLICANT:
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ID US-07-852-260-
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US-08-336-087
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                                                          e 87; DB 2; L
. No. 3.23e-02;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/011,644
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,40
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                             Sequence 5, Application US/08479400
Patent No. 5679784
GENERAL INFORMATION:
APPLICANT: Ladant, Daniel
APPLICANT: Leclerc, Claude
APPLICANT: Sebo, Peter
APPLICANT: Ullmann, Agnes
TITLE OF INVENTION: Recombinant Mu
TITLE OF INVENTION: Specific Immun
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  Henderson,
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
                                                                                                                                      PRT
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CHARACTERISTICS:
13 amino acids
      TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                      STANDARD;
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CHARACTERISTICS
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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larity 84.6%;
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TYPE: P
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. No. 3.23e-02;
Mismatches 0
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   Mismatches
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Ullmann, Agnes
INVENTION: Recombinant Mutan
INVENTION: Specific Immune R
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TITLE OF INVENTION: Specific Immune
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Fa
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/011,644
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Pred. No.
2; Misma
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                                                                                                                                                                                              Application US/08336087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
13 amino acids
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Sebo, Peter
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11; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08414926A
Patent No. 5721354
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTC
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro F
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Du
STREET: 1185 Avenue of
CITY: New York
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CITY: New
STATE: New
COUNTRY: U
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                                                      Sequence 2, Application US/C7852250
Patent No. 5525715
GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING
TITLE OF INVENTION: CDNA
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. No. 2.28e-01;
Mismatches C
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R: 36607-B-PCT-US
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COMPUTER: IBM PC COLOS/MS COMPUTER: Batentin Release #1.0, Ver SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/852,260
FILING DATE: 19920619
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-B-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
TVPE: AMINO ACID
TOWNS AND ACID
TOWNS AND ACID
TOWNS AND ACID
TOWNS AND ACID
                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; 25431833
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CANT: Weeks-Levy, Carolyn L
OF INVENTION: METHODS FOR
OF INVENTION: FROM CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08461503
                                       US/07852260
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larity 69.2%;
Conservative
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                                     Application
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APPLICANT:
TITLE OF IN
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,926A
FILING DATE: March 31, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL HUMAN CYTOMEGALOVIRUS
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                                                                                                                                                                                                                                                                                                                                e 79; DB 2; Len
l. No. 2.28e-01;
Mismatches 0;
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MATSUNAGA
PROTEIN-BOUND MAGNETIC PARTICLES
PROCESS OF PRODUCING THE SAME
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                                                                                                                       Length 876
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. No. 3.11e+01;
Mismatches 3
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Pred. No. 3.89e+01
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/529,600D FILING DATE: 18-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   N.W
                                                                                                   3870699 CN;
                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08529600D
Patent No. 5861285
GENERAL INFORMATION:
APPLICANT: Tadashi MATSUNAGA
TITLE OF INVENTION: PROTEIN-BOUND I
TITLE OF INVENTION: PROCESS OF PROI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SI
STREET: 1100 NEW YORK AVENUE, N.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     982549 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 6-248700
FILING DATE: 16-SEP-1994
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     Application US/08529600D
                                                                                                                       Score
Pred.
6; M
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LENGTH: 434 amino acids
TYPE: amino acid
  610-270-4478
610-270-5090
                                                  876 amino acids
amino acid
                                                                                                                                                                                                                           STANDARD;
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46827 MW;
                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 876 AA; 98538 MW;
                               N FOR SEQ ID NO:
CHARACTERISTICS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                       single
                                                                                                                       55.8%;
larity 25.0%;
Conservative
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                                                                      STRANDEDNESS:
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434 AA;
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                               INFORMATION FOR
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TELEPHONE:
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           TELEFAX:
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CITY: W
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Mismatches 2;
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                                31,822
FR: AVIR-011/00US
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APPLICATION NUMBER: US/08/785,071A
FILING DATE: 17-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9622617.0
FILING DATE: 27-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08785071A
Patent No. 5776750
GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5776750el tF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31355-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              /label= UL150
W; 2000477 CN;
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Pred. No.
2; Misma
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                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Smithkline Beec STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA COUNTRY: USA ZIP: 19406-0939 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATING SYSTEM: DOS SOFTWARE: FASTSEQ for Wind CURRENT APPLICATION DATA:
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                     NAME: Cserr, Luann
REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                   MW;
                                                                                                                                   protein
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trive
                                                                                                                                                                        NAME/KEY: Protein
LOCATION: 1..642
OTHER INFORMATION:
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GY: linear
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MOLECULE TYPE:
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ZIP: 48303
COMPUTER READABLE FORM:
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amino acid
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                                                                          USA
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TOPOLOGY: li
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SEQUENCE 132 AA;
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US-08-241-664B-14
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CITY: RO
STATE: M
COUNTRY:
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7.55e+01;
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      132
                                                                                                              STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MD
                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,298B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF175D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08409731A Patent No. 5658758 GENERAL INFORMATION:
                                                           US/08470298B
                                                                                                                                                                                                                                                                                                                                                           54;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08409731A
                                             Application US/08470298B
                                                                                                         CYTOSTATIN
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Pred. 3
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                                                                RAL INFORMATION:
PLICANT: NI, JIAN
PLICANT: GENTZ, REINER
TANT: YU, GUO-LIANG
                                                                                                                                                                             Floppy disk
      STANDARD;
                                                                                                                                                                                                                                                                                              amino acids
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                                                                             APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINEF
APPLICANT: YU, GUO-LIANG
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: CYTC
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENON
                                                                                                                                                                                                                                                                                                                                      P2 (I
                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 132 amino aci
                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         protein
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MEDIUM TYPE: Floppy
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larity 62.5%;
Conservative
                                                           11, Application . 5844081
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ORGANISM: MYE
JENCE 132 AA; 1
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                                                                                                                                                                                                                                                                                                                         MOLECULE IYPE:
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      US-08-470-298B-11
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                                                                                                                                                         COUNTRY:
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KFLAVWKI
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                                             11,
                                                                                                                                                                                                                                                                                                     TYPE:
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Patent No
GENERAL
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US-08-409-
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No. 7.55e+01;
Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, II
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                               LION DATA:
IMBER: US/08/409,731A
24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08241664B
Patent No. 5871909
GENERAL INFORMATION:
APPLICANT: Voorhees, John J.
APPLICANT: Astrom, Anders
APPLICANT: Tavakkol, Amir
TITLE OF INVENTION: HUMAN CRABP-I AN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierc
STREET: PO Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of America
                                                                                                                                                                                                                                                                  Release #1.0,
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Pred. No.
2; Misma
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ER: PF175
                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
14909 MW;
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CURRENT APPLICATION DATA
APPLICATION NUMBER: US
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US-07-879
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                                              FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 2115-00676COD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
TELEFAX: 287637
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
                           Version
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9.40e+01;
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REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 2115-00676DVF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                      \rho_{i}
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 48303

ZIP: 48303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,709B

FILING DATE: 06/06/95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Pierce,
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LK: US/08/241,664B
11, 1994
435
>ppy disk
> compatible
: PC-DOS/MS-DOS
tin Release #1.0, 1
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                                                                                                                                                                                                                                                                                                                                      se 14, Application US/08468709B
No. 5654137
AL INFORMATION:
LICANT: Astrom, Anders
                                                                                                                                                                                            Score 53;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                        Application US/08468709B
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Astrom, Anders
APPLICANT: Astrom, Anders
APPLICANT: Voorhees, John
APPLICANT: Pattersson, Ulrika
APPLICANT: Tavakkol, Amir
TITLE OF INVENTION: HUMAN CRABP
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey &
STREET: Po Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: United States of Ame
ZIP: 48303
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                                                                                                                                                                              CN;
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                                                                                                                                                                                                                                                                          STANDARD;
                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                              acids
                                                                                                                              FORMATION FOR SEQ ID NO: SEQUENCE CHARACIERISTICS
                                                                                                                                                                   : peptide
2950 MW: 3
TYPE: Floppy (ER: IBM PC com)
                                                                                                                                                                                            Similarity 41.7%;
5; Conservative
                         PatentIn
                                                                                                                                                            unknown
                                                                                                                                              amino
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                                                                                                                                                                    TYPE:
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3-468-709B-14
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KFLAVWKITYKD
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                                                                                                                                                                   MOLECULE TYPE
ENCE 25 AA;
                OPERATING SOFTWARE:
                                                                                                                                                             TOPOLOGY:
                                                                                                                                             LENGTH:
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                                                                                                                                                    TYPE
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Best Local
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                                                                                                                                                     Length
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,617A
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TENDING TO SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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No. 9.40e+01;
Mismatches 5
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Patent No. 5580775
GENERAL INFORMATION:
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Sui
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Affinity
                                                                                                                                                                                                                                                                                                    PRI;
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Pred.
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AMINO ACID
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XX: (810) 641-027(
287637
N FOR SEQ ID NO:
CHARACTERISTICS:
H: 25 amino acids
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NO
                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
ENCE 25 AA; 2950 MW;
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larity 41.7%;
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                   INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
LENGTH: 25 amino acid
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COUNTRY: U.S.
ZIP: 30309
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
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TYPE: AMINO
STRANDEDNESS:
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TISSUE TYPE:
FEATURE:
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LOCATION: 536..559
OTHER INFORMATION:
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LOCATION: 456..479
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 217..236
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 243..264
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 322..345
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 424..443
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 117..137
OTHER INFORMATION:
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LOCATION: 291..311
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 373..397
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 72..97
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 500..519
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: Domain
LOCATION: 46..65
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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NAME/KEY:
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          "Leucine zipper motif"
371 CN;
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                                       Length
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                                                No. 9.40e+01
Mismatches
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                                       DB
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879617
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                Sequence 9, Application US/08753985
Patent No. 5759788
GENERAL INFORMATION:
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity
                                                                                                                                                                                                                                                                                                                                                                                                                         53,985
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,98
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                                     Score 53;
Pred. No.
1; Misma
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Street,
          /note= "Le:
MW; 2226371
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03-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: ENTELECOMMUNICATION INFORMATION IELEPHONE: 404-815-6558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 404-515 VINFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: TRNGTH: 635 amino acids
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                                                                                                                                                                                                                                                                                                  SSEE: Kilpatrick & R. 1100 Peachtree & Atlanta
                                                                                                                                                                                                                                                                                                         Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick
STREET: 1100 Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 FORM:
                                      Similarity 85.7%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brain
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LOCATION: 46..65
OTHER INFORMATION:
LOCATION: 97..98
OTHER INFORMATION:
ICE 635 AA; 70857
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: HYPOTHETICAL:
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US-08-753-985
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                                                                    /note= "Proposed domain."
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                                                                                  FEATURE:
NAME/KEY: Domain
LOCATION: 217..236
OTHER INFORMATION:
FEATURE:
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LOCATION: 500..519
OTHER INFORMATION:
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LOCATION: 322..345
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LOCATION: 536..559
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LOCATION: 243..264
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LOCATION: 291..311
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LOCATION: 373..397
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LOCATION: 97..98
OTHER INFORMATION:
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FEATURE:
NAME/KEY: Domain
LOCATION: 72..97
OTHER INFORMATION:
OTHER INFORMATION:
                                                    NAME/KEY: Domain
LOCATION: 117..137
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LOCATION: 456..479
OTHER INFORMATION:
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LOCATION: 90..91
OTHER INFORMATION:
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LOCATION: 76..77
OTHER INFORMATION:
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LOCATION: 83..84
OTHER INFORMATION:
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                      Gaps
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 Length 635;
                    Indels
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 e 53; DB 2; L
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Mismatches 0
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TELEPHONE: 404-815-6508
TELEFRAX: 404-815-6558
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 667 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/879617

FILING DATE: 01-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: EMU109
                                                                                                                                                                                                                                                                                                                                                           ___ #1.0,
__ATA:
US/08/753,985
03-DEC-1996
N: 536
                                                                                                                                                                                                                                                                                                            ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                       Sequence 8, Application US/08753985
Patent No. 5759788
GENERAL INFORMATION:
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affini NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody STREET: 1100 Peachtree Street, 3
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
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 Score 53;
Pred. No.
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51.0%;
larity 85.7%;
Conservative
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FILING DATE: 03-DEC
CLASSIFICATION: 530
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LOCATION: 76..95
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MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
FRAGMENT TYPE:
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TELEFAX: 40'
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OTHER INFORMATION: 7
OTHER INFORMATION: FEATURE:
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NAME/KEY: Region
LOCATION: 269..270
OTHER INFORMATION:
     NAME/KEY: Domain
LOCATION: 103..127
OTHER INFORMATION:
FEATURE:
NAME/KEY: Domain
LOCATION: 147..167
OTHER INFORMATION:
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LOCATION: 530..549
OTHER INFORMATION:
FEATURE:
NAME/KEY: Domain
LOCATION: 567..589
OTHER INFORMATION:
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LOCATION: 106..127
OIHER INFORMATION: ,
                                                              FEATURE:
NAME/KEY: Domain
LOCATION: 247..266
OTHER INFORMATION:
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NAME/KEY: Domain
LOCATION: 404..427
OTHER INFORMATION:
FEATURE:
NAME/KEY: Domain
LOCATION: 454..473
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LOCATION: 212..213
OIHER INFORMATION:
OIHER INFORMATION:
                                                                                                                                  LOCATION: 321..341
OTHER INFORMATION:
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LOCATION: 71..72
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 272..294
OTHER INFORMATION:
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LOCATION: 353..375
OTHER INFORMATION:
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LOCATION: 454..473
OTHER INFORMATION:
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LOCATION: 487..509
OTHER INFORMATION:
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LOCATION: 44..45
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
LOCATION:
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SQ SEQUENCE 667 AA; 74584 MW; 2468833 CN;

Query Match

Best Local Similarity 85.7%; Pred. No. 9.40e+01;

Matches 6; Conservative 1; Mismatches 0; Indels 0;

Db 136 LAVWKIS 142

QY 3 LAVWKIT 9
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Gaps

Search completed: Tue Aug 17 16:04:43 1999 Job time: 7 secs.

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